SEQUENCE LISTING

<110> Wagner, et al.

<120> GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM

<130> 1505-54357

<140> 09/513,057
<141> 2000-02-24

<160> 68

<170> PatentIn version 3.1

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Met Lys Arg Gly
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Lys Asp Glu Glu Lys Ile Leu Glu Pro Met Phe Pro Arg Leu His Val
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Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met
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Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser Thr Leu Val His Pro
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His Leu Asp Ser Ser Ala Ala Asn Gln Ala Thr Glu Lys Phe Val Ser
85                  90                  95                  100

caa atg tcc ttc atg gaa aat gtg aga tct tcg gca cag cat gat cag      631
Gln Met Ser Phe Met Glu Asn Val Arg Ser Ser Ala Gln His Asp Gln
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agg aaa atg gtg aga gag gaa gaa gat ttt gca gtt cca gta tat att      679
Arg Lys Met Val Arg Glu Glu Glu Asp Phe Ala Val Pro Val Tyr Ile
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aac tca aga aga tct cag tct cat ggc aga acc aag agt ggt att gag      727
Asn Ser Arg Arg Ser Gln Ser His Gly Arg Thr Lys Ser Gly Ile Glu
        135                 140                 145

aag gaa aaa cac acc cca atg gtg gca cct agc tct cat cac tcc att      775
Lys Glu Lys His Thr Pro Met Val Ala Pro Ser Ser His His Ser Ile
    150                 155                 160

cga ttt caa gaa gtg aat cag aca ggc tca aag caa aac gta tgt ttg      823
Arg Phe Gln Glu Val Asn Gln Thr Gly Ser Lys Gln Asn Val Cys Leu
165                 170                 175                 180

gct act tgt tca aaa cct gaa gtt agg gat cag gtc aag gcg aat gca      871
Ala Thr Cys Ser Lys Pro Glu Val Arg Asp Gln Val Lys Ala Asn Ala
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agg tca ggt ggc ttt gta atc tct tta gat gta tca gtc aca gag gag      919
Arg Ser Gly Gly Phe Val Ile Ser Leu Asp Val Ser Val Thr Glu Glu
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att gat ctc gaa aaa tca gca tca agt cat gat aga gta aat gat tat      967
Ile Asp Leu Glu Lys Ser Ala Ser Ser His Asp Arg Val Asn Asp Tyr
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aat gct tcc ttg aga caa gag tct aga aat cgg tta tac cga gat ggt     1015
Asn Ala Ser Leu Arg Gln Glu Ser Arg Asn Arg Leu Tyr Arg Asp Gly
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ggc aaa act cgt ctg aag gac act gat aat gga gct gaa tct cac ttg     1063
Gly Lys Thr Arg Leu Lys Asp Thr Asp Asn Gly Ala Glu Ser His Leu
245                 250                 255                 260

gca acg gaa aat cat tca caa gag ggt cat ggc agt cct gaa gac att     1111
Ala Thr Glu Asn His Ser Gln Glu Gly His Gly Ser Pro Glu Asp Ile
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gat aat gat cgt gaa tac agc aaa agc aga gca tgc gcc tct ctg cag     1159
Asp Asn Asp Arg Glu Tyr Ser Lys Ser Arg Ala Cys Ala Ser Leu Gln
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cag ata aat gaa gag gca agt gat gac gtt tct gat gat tcg atg gtg     1207
Gln Ile Asn Glu Glu Ala Ser Asp Asp Val Ser Asp Asp Ser Met Val
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Asp Ser Ile Ser Ser Ile Asp Val Ser Pro Asp Asp Val Val Gly Ile
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tta ggt caa aaa cgt ttc tgg aga gca agg aaa gcc att gcc aat caa     1303
Leu Gly Gln Lys Arg Phe Trp Arg Ala Arg Lys Ala Ile Ala Asn Gln
325                 330                 335                 340

caa aga gta ttt gct gtt caa cta ttt gag ttg cac aga ctg att aag     1351
Gln Arg Val Phe Ala Val Gln Leu Phe Glu Leu His Arg Leu Ile Lys
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gtt caa aaa ctt att gct gca tca ccg gat ctc ttg ctc gat gag atc     1399
Val Gln Lys Leu Ile Ala Ala Ser Pro Asp Leu Leu Leu Asp Glu Ile
            360                 365                 370

agt ttt ctt gga aaa gtt tct gct aaa agc tat cca gtg aag aag ctc     1447
Ser Phe Leu Gly Lys Val Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu
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ctt cca tca gaa ttt ctg gta aag cct cct cta cca cat gtt gtc gtc     1495
Leu Pro Ser Glu Phe Leu Val Lys Pro Pro Leu Pro His Val Val Val
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aaa caa agg ggt gac tcg gag aag act gac caa cat aaa atg gaa agc     1543
Lys Gln Arg Gly Asp Ser Glu Lys Thr Asp Gln His Lys Met Glu Ser
405                 410                 415                 420

tca gct gag aac gta gtt ggg agg ttg tca aat caa ggt cat cat caa     1591
Ser Ala Glu Asn Val Val Gly Arg Leu Ser Asn Gln Gly His His Gln
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caa tcc aac tac atg cct ttt gca aac aac cca ccg gct tca ccg gct     1639
Gln Ser Asn Tyr Met Pro Phe Ala Asn Asn Pro Pro Ala Ser Pro Ala
            440                 445                 450

cca aat gga tat tgc ttt cct cct cag cct cct cct tca gga aat cat     1687
Pro Asn Gly Tyr Cys Phe Pro Pro Gln Pro Pro Pro Ser Gly Asn His
        455                 460                 465

cag caa tgg ttg atc cct gta atg tct ccc tcg gaa gga ctg ata tac     1735
Gln Gln Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr
    470                 475                 480

aag cct cac cca ggt atg gca cac acg ggg cat tat gga gga tat tat     1783
Lys Pro His Pro Gly Met Ala His Thr Gly His Tyr Gly Gly Tyr Tyr
485                 490                 495                 500

ggt cat tat atg cct aca cca atg gta atg cct caa tat cac ccc ggc     1831
Gly His Tyr Met Pro Thr Pro Met Val Met Pro Gln Tyr His Pro Gly
                505                 510                 515

atg gga ttc cca cct cct ggt aat ggc tac ttc cct cca tat gga atg     1879
Met Gly Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Met
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Met Pro Thr Ile Met Asn Pro Tyr Cys Ser Ser Gln Gln Gln Gln Gln
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caa caa ccc aat gag caa atg aac cag ttt gga cat cct gga aat ctt     1975
Gln Gln Pro Asn Glu Gln Met Asn Gln Phe Gly His Pro Gly Asn Leu
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cag aac acc caa caa caa caa cag aga tct gat aat gaa cct gct cca     2023
Gln Asn Thr Gln Gln Gln Gln Gln Arg Ser Asp Asn Glu Pro Ala Pro
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cag caa cag caa cag cca aca aag tct tat ccg cga gca aga aag agc     2071
Gln Gln Gln Gln Gln Pro Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser
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agg caa ggg agc aca gga agc agt cca agt ggg cca cag gga atc tct     2119
Arg Gln Gly Ser Thr Gly Ser Ser Pro Ser Gly Pro Gln Gly Ile Ser
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ggt agc aag tcc ttt cgg cca ttc gca gcc gtt gat gag gac agc aac     2167
Gly Ser Lys Ser Phe Arg Pro Phe Ala Ala Val Asp Glu Asp Ser Asn
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Ile Asn Asn Ala Pro Glu Gln Thr Met Thr Thr Thr Thr Thr Thr Thr
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aga aca act gtt act cag aca aca aga gat ggg gga gga gtg acg aga     2263
Arg Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Gly Gly Val Thr Arg
645                 650                 655                 660

gtg ata aag gtg gta cct cac aac gca aag ctc gcg agt gag aat gct     2311
Val Ile Lys Val Val Pro His Asn Ala Lys Leu Ala Ser Glu Asn Ala
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gcc aga att ttc cag tca ata caa gaa gaa cgt aaa cgc tat gac tcc     2359
Ala Arg Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys Arg Tyr Asp Ser
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Ser Lys Pro
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Phe Gly Asp His Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser Thr
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Leu Val His Pro Gly Pro Ser Ser Gln Pro Cys Gly Val Glu Arg Asn
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Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Asn Gln Ala Thr Glu
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Lys Phe Val Ser Gln Met Ser Phe Met Glu Asn Val Arg Ser Ser Ala
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Gln His Asp Gln Arg Lys Met Val Arg Glu Glu Glu Asp Phe Ala Val
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Pro Val Tyr Ile Asn Ser Arg Arg Ser Gln Ser His Gly Arg Thr Lys
    130                 135                 140

Ser Gly Ile Glu Lys Glu Lys His Thr Pro Met Val Ala Pro Ser Ser
145                 150                 155                 160

His His Ser Ile Arg Phe Gln Glu Val Asn Gln Thr Gly Ser Lys Gln
                165                 170                 175

Asn Val Cys Leu Ala Thr Cys Ser Lys Pro Glu Val Arg Asp Gln Val
            180                 185                 190

Lys Ala Asn Ala Arg Ser Gly Gly Phe Val Ile Ser Leu Asp Val Ser
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Val Thr Glu Glu Ile Asp Leu Glu Lys Ser Ala Ser Ser His Asp Arg
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Val Asn Asp Tyr Asn Ala Ser Leu Arg Gln Glu Ser Arg Asn Arg Leu
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Tyr Arg Asp Gly Gly Lys Thr Arg Leu Lys Asp Thr Asp Asn Gly Ala
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Glu Ser His Leu Ala Thr Glu Asn His Ser Gln Glu Gly His Gly Ser
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Pro Glu Asp Ile Asp Asn Asp Arg Glu Tyr Ser Lys Ser Arg Ala Cys
        275                 280                 285

Ala Ser Leu Gln Gln Ile Asn Glu Glu Ala Ser Asp Asp Val Ser Asp
    290                 295                 300

Asp Ser Met Val Asp Ser Ile Ser Ser Ile Asp Val Ser Pro Asp Asp
305                 310                 315                 320

Val Val Gly Ile Leu Gly Gln Lys Arg Phe Trp Arg Ala Arg Lys Ala
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Ile Ala Asn Gln Gln Arg Val Phe Ala Val Gln Leu Phe Glu Leu His
            340                 345                 350

Arg Leu Ile Lys Val Gln Lys Leu Ile Ala Ala Ser Pro Asp Leu Leu
        355                 360                 365

Leu Asp Glu Ile Ser Phe Leu Gly Lys Val Ser Ala Lys Ser Tyr Pro
    370                 375                 380

Val Lys Lys Leu Leu Pro Ser Glu Phe Leu Val Lys Pro Pro Leu Pro
385                 390                 395                 400

His Val Val Val Lys Gln Arg Gly Asp Ser Glu Lys Thr Asp Gln His
                405                 410                 415

Lys Met Glu Ser Ser Ala Glu Asn Val Val Gly Arg Leu Ser Asn Gln
            420                 425                 430

Gly His His Gln Gln Ser Asn Tyr Met Pro Phe Ala Asn Asn Pro Pro
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Ala Ser Pro Ala Pro Asn Gly Tyr Cys Phe Pro Pro Gln Pro Pro Pro
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Ser Gly Asn His Gln Gln Trp Leu Ile Pro Val Met Ser Pro Ser Glu
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Gly Leu Ile Tyr Lys Pro His Pro Gly Met Ala His Thr Gly His Tyr
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Gly Gly Tyr Tyr Gly His Tyr Met Pro Thr Pro Met Val Met Pro Gln
            500                 505                 510

Tyr His Pro Gly Met Gly Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro
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Pro Tyr Gly Met Met Pro Thr Ile Met Asn Pro Tyr Cys Ser Ser Gln
    530                 535                 540

Gln Gln Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Gln Phe Gly His
545                 550                 555                 560

Pro Gly Asn Leu Gln Asn Thr Gln Gln Gln Gln Gln Arg Ser Asp Asn
                565                 570                 575

Glu Pro Ala Pro Gln Gln Gln Gln Gln Pro Thr Lys Ser Tyr Pro Arg
            580                 585                 590

Ala Arg Lys Ser Arg Gln Gly Ser Thr Gly Ser Ser Pro Ser Gly Pro
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Gln Gly Ile Ser Gly Ser Lys Ser Phe Arg Pro Phe Ala Ala Val Asp
    610                 615                 620

Glu Asp Ser Asn Ile Asn Asn Ala Pro Glu Gln Thr Met Thr Thr Thr
625                 630                 635                 640

Thr Thr Thr Thr Arg Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Gly
                645                 650                 655

Gly Val Thr Arg Val Ile Lys Val Val Pro His Asn Ala Lys Leu Ala
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gagtg atg aag aga ggg aaa gat gag gag aag ata ttg gaa cct atg ttt 470
Met Lys Arg Gly Lys Asp Glu Glu Lys Ile Leu Glu Pro Met Phe
1 5 10 15

cct cgg ctt cat gtg aat gat gca gat aaa gga ggg cct aga gct cct 518
Pro Arg Leu His Val Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala Pro
20 25 30

cct aga aac aag atg gct ctt tat gag cag ctt agt att cct tct cag 566
Pro Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln
35 40 45

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Arg Phe Gly Asp His Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser
50 55 60

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Thr Leu Val His Pro Gly Pro Ser Ser Gln
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gaa aga aac tta tct gtc cag cat ctt gat tct tca gcc gca aac caa      1066
Glu Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Asn Gln
        80                  85                  90

gca act gag aag ttt gtc tcc caa atg tcc ttc atg gaa aat gtg aga      1114
Ala Thr Glu Lys Phe Val Ser Gln Met Ser Phe Met Glu Asn Val Arg
    95                  100                 105

tct tcg gca cag cat gat cag agg aaa atg gtg aga gag gaa gaa gat      1162
Ser Ser Ala Gln His Asp Gln Arg Lys Met Val Arg Glu Glu Glu Asp
110                 115                 120                 125

ttt gca gtt cca gta tat att aac tca aga aga tct cag tct cat ggc      1210
Phe Ala Val Pro Val Tyr Ile Asn Ser Arg Arg Ser Gln Ser His Gly
                130                 135                 140

aga acc aag agt ggt att gag aag gaa aaa cac acc cca atg gtg gca      1258
Arg Thr Lys Ser Gly Ile Glu Lys Glu Lys His Thr Pro Met Val Ala
            145                 150                 155

cct agc tct cat cac tcc att cga ttt caa gaa gtg aat cag aca ggc      1306
Pro Ser Ser His His Ser Ile Arg Phe Gln Glu Val Asn Gln Thr Gly
        160                 165                 170

tca aag caa aac gta tgt ttg gct act tgt tca aaa cct gaa gtt agg      1354
Ser Lys Gln Asn Val Cys Leu Ala Thr Cys Ser Lys Pro Glu Val Arg
    175                 180                 185

gat cag gtc aag gcg aat gca agg tca ggt ggc ttt gta atc tct tta      1402
Asp Gln Val Lys Ala Asn Ala Arg Ser Gly Gly Phe Val Ile Ser Leu
190                 195                 200                 205

gat gta tca gtc aca gag gag att gat ctc gaa aaa tca gca tca agt      1450
Asp Val Ser Val Thr Glu Glu Ile Asp Leu Glu Lys Ser Ala Ser Ser
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His Asp Arg Val Asn Asp Tyr Asn Ala Ser Leu Arg Gln Glu Ser Arg
            225                 230                 235

aat cgg tta tac cga gat ggt ggc aaa act cgt ctg aag gac act gat      1546
Asn Arg Leu Tyr Arg Asp Gly Gly Lys Thr Arg Leu Lys Asp Thr Asp
        240                 245                 250

aat gga gct gaa tct cac ttg gca acg gaa aat cat tca caa gag ggt      1594
Asn Gly Ala Glu Ser His Leu Ala Thr Glu Asn His Ser Gln Glu Gly
    255                 260                 265

cat ggc agt cct gaa gac att gat aat gat cgt gaa tac agc aaa agc      1642
His Gly Ser Pro Glu Asp Ile Asp Asn Asp Arg Glu Tyr Ser Lys Ser
270                 275                 280                 285

aga gca tgc gcc tct ctg cag cag ata aat gaa gag gca agt gat gac      1690
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gtt tct gat gat tcg atg gtg gat tct ata tcc agc ata gat gtc tct     1738
Val Ser Asp Asp Ser Met Val Asp Ser Ile Ser Ser Ile Asp Val Ser
            305                 310                 315

ccc gat gat gtt gtg ggt ata tta ggt caa aaa cgt ttc tgg aga gca     1786
Pro Asp Asp Val Val Gly Ile Leu Gly Gln Lys Arg Phe Trp Arg Ala
        320                 325                 330

agg aaa gcc att gcc aa  gtaagttcac tagaaattta cagtttggtt            1833
Arg Lys Ala Ile Ala Asn
    335

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                                                        Gln Lys


ctt att gct gca tca ccg gat ctc ttg ctc gat gag atc agt ttt ctt     3182
Leu Ile Ala Ala Ser Pro Asp Leu Leu Leu Asp Glu Ile Ser Phe Leu
360                 365                 370                 375

gga aaa gtt tct gct aaa agc tat cca gtg aag aag ctc ctt cca tca     3230
Gly Lys Val Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Leu Pro Ser
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gaa ttt ctg gta aag cct cct cta cca cat gtt gtc gtc aaa caa agg     3278
Glu Phe Leu Val Lys Pro Pro Leu Pro His Val Val Val Lys Gln Arg
            395                 400                 405

ggt gac tcg gag aag act gac caa cat aaa atg gaa agc tca gct gag     3326
Gly Asp Ser Glu Lys Thr Asp Gln His Lys Met Glu Ser Ser Ala Glu
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aac gta gtt ggg agg ttg tca aat caa ggt cat cat caa caa tcc aac     3374
Asn Val Val Gly Arg Leu Ser Asn Gln Gly His His Gln Gln Ser Asn
    425                 430                 435

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Tyr Met Pro Phe Ala Asn Asn Pro Pro Ala Ser Pro Ala Pro Asn Gly
440                 445                 450                 455

tat tgc ttt cct cct cag cct cct cct tca gga aat cat cag caa tgg     3470
Tyr Cys Phe Pro Pro Gln Pro Pro Pro Ser Gly Asn His Gln Gln Trp
                460                 465                 470

ttg atc cct gta atg tct ccc tcg gaa gga ctg ata tac aag cct cac     3518
Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro His
            475                 480                 485

cca ggt atg gca cac acg ggg cat tat gga gga tat tat ggt cat tat     3566
Pro Gly Met Ala His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His Tyr
        490                 495                 500

atg cct aca cca atg gta atg cct caa tat cac ccc ggc atg gga ttc     3614
Met Pro Thr Pro Met Val Met Pro Gln Tyr His Pro Gly Met Gly Phe
    505                 510                 515

cca cct cct ggt aat ggc tac ttc cct cca tat gga atg atg ccc acc     3662
Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Met Met Pro Thr
520                 525                 530                 535

ata atg aac cca tat tgt tca agc caa caa caa caa caa caa caa ccc     3710
Ile Met Asn Pro Tyr Cys Ser Ser Gln Gln Gln Gln Gln Gln Gln Pro
                540                 545                 550

aat gag caa atg aac cag ttt gga cat cct gga aat ctt cag aac acc     3758
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Asn Glu Gln Met Asn Gln Phe Gly His Pro Gly Asn Leu Gln Asn Thr
            555                 560                 565

caa caa caa caa cag aga tct gat aat gaa cct gct cca cag caa cag     3806
Gln Gln Gln Gln Gln Arg Ser Asp Asn Glu Pro Ala Pro Gln Gln Gln
        570                 575                 580

caa cag cca aca aag tct tat ccg cga gca aga aag agc agg caa ggg     3854
Gln Gln Pro Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln Gly
    585                 590                 595

agc aca gga agc agt cca agt ggg cca cag gga atc tct ggt agc aag     3902
Ser Thr Gly Ser Ser Pro Ser Gly Pro Gln Gly Ile Ser Gly Ser Lys
600                 605                 610                 615

tcc ttt cgg cca ttc gca gcc gtt gat gag gac agc aac atc aac aat     3950
Ser Phe Arg Pro Phe Ala Ala Val Asp Glu Asp Ser Asn Ile Asn Asn
                620                 625                 630

gca cct gag caa acg atg aca aca acc aca acg acg aca aga aca act     3998
Ala Pro Glu Gln Thr Met Thr Thr Thr Thr Thr Thr Thr Arg Thr Thr
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gtt act cag aca aca aga gat ggg gga gga gtg acg aga gtg ata aag     4046
Val Thr Gln Thr Thr Arg Asp Gly Gly Gly Val Thr Arg Val Ile Lys
        650                 655                 660

gtg gta cct cac aac gca aag ctc gcg agt gag aat gct gcc aga att     4094
Val Val Pro His Asn Ala Lys Leu Ala Ser Glu Asn Ala Ala Arg Ile
    665                 670                 675

ttc cag tca ata caa gaa gaa cgt aaa cgc tat gac tcc tct aag cct     4142
Phe Gln Ser Ile Gln Glu Glu Arg Lys Arg Tyr Asp Ser Ser Lys Pro
680                 685                 690                 695

taatcctctc tatgcgtatt gtacttgata tgtattttac aaaattagaa aaattgtgat   4202

agatgttatc ctcaatata                                               4221
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<210> 4
<211> 2088
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<213> Arabidopsis thaliana

<400> 4

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cagcttagta ttccttctca gaggtttggt gatcatggaa cgatgaattc tcgtagtaac    180

aacacaagca ctttggttca tcctggacca tctagtcagc cttgtggtgt ggaaagaaac    240

ttatctgtcc agcatcttga ttcttcagcc gcaaaccaag caactgagaa gtttgtctcc    300

caaatgtcct tcatggaaaa tgtgagatct tcggcacagc atgatcagag gaaaatggtg    360
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catcactcca ttcgatttca agaagtgaat cagacaggct caaagcaaaa cgtatgtttg 540

gctacttgtt caaaacctga agttagggat caggtcaagg cgaatgcaag gtcaggtggc 600

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gcaacggaaa atcattcaca agagggtcat ggcagtcctg aagacattga taatgatcgt 840

gaatacagca aaagcagagc atgcgcctct ctgcagcaga taaatgaaga ggcaagtgat 900

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ggtcattata tgcctacacc aatggtaatg cctcaatatc accccggcat gggattccca 1560

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gcagccgttg atgaggacag caacatcaac aatgcacctg agcaaacgat gacaacaacc 1920

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gtgataaagg tggtacctca caacgcaaag ctcgcgagtg agaatgctgc cagaattttc 2040

cagtcaatac aagaagaacg taaacgctat gactcctcta agccttaa 2088

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<211> 4071
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<213> Arabidopsis thaliana

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gtacacaatc caaattgcaa aagagagata ctgcaaatga tctaatcaaa actcatgcat 180

tctacagttc cataagacat ttcaaatcac taatctgaag aaatatgatg cattaataac 240

aaatatttga taactaaaca gacatttgga tcagaaatga agttaaatta agcatttaat 300

tgcttaataa tttaattgat tgattcaaag gcgtaataac acaaaattct tcgggggaat 360

ttgaagggat agagcaaatc gcttagggta aaatgaaaac agcgataagt aacgaattat 420

caaagtctga gttaagaatc aggaaattga gggattgaag aagaataaag ggacctggtt 480

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cccaataaaa accacgatcc atttttattt ggacatttaa tatttaatta ttttaaatta 720

gaaaataatt acacgaatta ctaaattgta taatatgata ttaaaaaatt aagtgttatt 780

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<220>
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<400> 6
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<210> 7
<211> 25
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<400> 7
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<210> 8
<211> 24
<212> DNA
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<220>
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ttaaggctta gaggagtcat agcgt 25

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agtaagagag ggaaagatga gg 22

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<223>

<400> 12

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Met Lys Arg Gly Lys Asp Asp Glu Lys Ile Leu Glu Pro Met Phe Pro
1               5                  10                  15

aga ctt cat gtg aat gat gca gat aaa gga gga cct aga gct cct cct       96
Arg Leu His Val Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala Pro Pro
            20                  25                  30

aga aac aag atg gct ctt tat gag cag ctt agt atc cct tct cag agg      144
Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
        35                  40                  45

ttt ggt gat cat gga aat ttg tct ctg agt tct cgt agt aac aac aca      192
Phe Gly Asp His Gly Asn Leu Ser Leu Ser Ser Arg Ser Asn Asn Thr
    50                  55                  60

agt act ttg gtt cac cct gga cca tct aat cag cag tct tgt ggt gtg      240
Ser Thr Leu Val His Pro Gly Pro Ser Asn Gln Gln Ser Cys Gly Val
65                  70                  75                  80

gaa cga aac tta tct gtc cag cat ctt gat tct tca gct gca gtc cat      288
Glu Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Val His
                85                  90                  95

gta act gag aat ttt gtc tcc caa atg ccc ttc atg gaa aat atg aga      336
Val Thr Glu Asn Phe Val Ser Gln Met Pro Phe Met Glu Asn Met Arg
            100                 105                 110

tct ttg gca aag cat gat cag agg aaa aca gta aga gag gaa gat gac      384
Ser Leu Ala Lys His Asp Gln Arg Lys Thr Val Arg Glu Glu Asp Asp
        115                 120                 125

ttt gca gtt cca gtg ttt gtt aac tca aga aga ttc cag agt cat ggt      432
Phe Ala Val Pro Val Phe Val Asn Ser Arg Arg Phe Gln Ser His Gly
    130                 135                 140

agt acc aag agt ggg att gtg att gaa aaa cac acg aca ttg gct act      480
Ser Thr Lys Ser Gly Ile Val Ile Glu Lys His Thr Thr Leu Ala Thr
145                 150                 155                 160

tgt tca aaa ctt gtt aga gat aag gtg aag atg aac gca aag tca ggt      528
Cys Ser Lys Leu Val Arg Asp Lys Val Lys Met Asn Ala Lys Ser Gly
                165                 170                 175

ggc ttt ata gat tta tca tca aca gag gaa gtg gat ctc gaa aaa tca      576
Gly Phe Ile Asp Leu Ser Ser Thr Glu Glu Val Asp Leu Glu Lys Ser
            180                 185                 190

gca tca agt tat gac aga gta aat gat tgt aat tct tcc ttg aga caa      624
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Ala Ser Ser Tyr Asp Arg Val Asn Asp Cys Asn Ser Ser Leu Arg Gln
        195                 200                 205

gag tct aga aat aag tta tac cga gat ggt ggc gaa gct cat atg aag      672
Glu Ser Arg Asn Lys Leu Tyr Arg Asp Gly Gly Glu Ala His Met Lys
    210                 215                 220

gac act gct aat aga gtt gaa tct cac ttg gta acg gaa agt cat tct      720
Asp Thr Ala Asn Arg Val Glu Ser His Leu Val Thr Glu Ser His Ser
225                 230                 235                 240

gag gag ggt cat ggc agt cct gat gat gat gac aac ggt cat gaa tac      768
Glu Glu Gly His Gly Ser Pro Asp Asp Asp Asp Asn Gly His Glu Tyr
                245                 250                 255

tgc aga agc aga gga ggc gtc tct cta cag cag ata aat gaa gag gca      816
Cys Arg Ser Arg Gly Gly Val Ser Leu Gln Gln Ile Asn Glu Glu Ala
            260                 265                 270

agt gat gac gtt tct gat aat tcg atg gtg gat tct ata tcc agc ata      864
Ser Asp Asp Val Ser Asp Asn Ser Met Val Asp Ser Ile Ser Ser Ile
        275                 280                 285

gat gtt tct cct gat gat gtt gtg gga gca tta ggt caa aaa cgt ttc      912
Asp Val Ser Pro Asp Asp Val Val Gly Ala Leu Gly Gln Lys Arg Phe
    290                 295                 300

tgg agg gca agg aag gct att acc aat caa caa aga gta ttt gct gtt      960
Trp Arg Ala Arg Lys Ala Ile Thr Asn Gln Gln Arg Val Phe Ala Val
305                 310                 315                 320

caa cta ttt gag ttg cac aga ctg att aag gtt caa aga ctt att gct     1008
Gln Leu Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg Leu Ile Ala
                325                 330                 335

gca tca ccg gat atc gtg ctc gac gaa atc aat tac ctt gga aaa gtt     1056
Ala Ser Pro Asp Ile Val Leu Asp Glu Ile Asn Tyr Leu Gly Lys Val
            340                 345                 350

tct gct aaa agc tat cca gtg aag aag ctc gtt cca tca gaa ttt atc     1104
Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Val Pro Ser Glu Phe Ile
        355                 360                 365

gta aag cct cct cta cca caa gtt gtc gtc aac aaa cag cac agg agc     1152
Val Lys Pro Pro Leu Pro Gln Val Val Val Asn Lys Gln His Arg Ser
    370                 375                 380

gac tcc gaa aag act gac caa cat aaa atg gaa tgc tca gct gag aat     1200
Asp Ser Glu Lys Thr Asp Gln His Lys Met Glu Cys Ser Ala Glu Asn
385                 390                 395                 400

gtt gtt ggt agg ttg tca aac caa gga cat cat cat aat cat caa cct     1248
Val Val Gly Arg Leu Ser Asn Gln Gly His His His Asn His Gln Pro
                405                 410                 415

tcc aac tac atg cct ttt cca agc aac cca ccc gct tca cca gct gta     1296
Ser Asn Tyr Met Pro Phe Pro Ser Asn Pro Pro Ala Ser Pro Ala Val
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            420                 425                 430

aac gga tgt tgc tat cct cct cag cct cct cct tca gga aac cag caa     1344
Asn Gly Cys Cys Tyr Pro Pro Gln Pro Pro Pro Ser Gly Asn Gln Gln
        435                 440                 445

tgg tta atc cct gtt atg tct cct tct gaa gga ctt ata tac aag cct     1392
Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro
    450                 455                 460

cat cct ggt atg gga cac acg ggg cac tac gga gga tat tat ggt cat     1440
His Pro Gly Met Gly His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His
465                 470                 475                 480

ttt atg cct ccg ccg atg gta atg cct ccg ttt cat ccg ggc atg gga     1488
Phe Met Pro Pro Pro Met Val Met Pro Pro Phe His Pro Gly Met Gly
                485                 490                 495

ttc cca cct cct ggt aat ggc tac ttc cct cct tat ggt gta atc cca     1536
Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Val Ile Pro
            500                 505                 510

gcc atg atg aac cct tat ggt cca ggc caa caa caa caa caa caa cca     1584
Ala Met Met Asn Pro Tyr Gly Pro Gly Gln Gln Gln Gln Gln Gln Pro
        515                 520                 525

caa gcc aat gaa caa acg aat cag ttt ggg tat tct ggg aat ctt cag     1632
Gln Ala Asn Glu Gln Thr Asn Gln Phe Gly Tyr Ser Gly Asn Leu Gln
    530                 535                 540

aac aac acc cat caa gaa agc tcc gtt aat gaa gct gct cct cca cag     1680
Asn Asn Thr His Gln Glu Ser Ser Val Asn Glu Ala Ala Pro Pro Gln
545                 550                 555                 560

gaa cca cta aca aag tct tat ccg cgg gct aga aag agc agg caa gtg     1728
Glu Pro Leu Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln Val
                565                 570                 575

agc aca gca agc agt gca agt ggg cga gag gga atc tcc ggt agc act     1776
Ser Thr Ala Ser Ser Ala Ser Gly Arg Glu Gly Ile Ser Gly Ser Thr
            580                 585                 590

tcc ttt cgt cca ttc tca gcc gtt gat gag gat aac aac gat aac aac     1824
Ser Phe Arg Pro Phe Ser Ala Val Asp Glu Asp Asn Asn Asp Asn Asn
        595                 600                 605

aac gac gca cct gat caa atg atg aca acc acc acg acc acg aca aga     1872
Asn Asp Ala Pro Asp Gln Met Met Thr Thr Thr Thr Thr Thr Thr Arg
    610                 615                 620

aca act gtt act cag aca aca aga gat gga gga gaa gtg acg aga gtg     1920
Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Gly Glu Val Thr Arg Val
625                 630                 635                 640

ata aag ggg ttc ctc aca atg cga agc tcg cta gtg aga a               1960
Ile Lys Gly Phe Leu Thr Met Arg Ser Ser Leu Val Arg
                645                 650
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<210> 13
<211> 653
<212> PRT
<213> Cardamine oligosperma

<400> 13

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Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
35 40 45

Phe Gly Asp His Gly Asn Leu Ser Leu Ser Ser Arg Ser Asn Asn Thr
50 55 60

Ser Thr Leu Val His Pro Gly Pro Ser Asn Gln Gln Ser Cys Gly Val
65 70 75 80

Glu Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Val His
85 90 95

Val Thr Glu Asn Phe Val Ser Gln Met Pro Phe Met Glu Asn Met Arg
100 105 110

Ser Leu Ala Lys His Asp Gln Arg Lys Thr Val Arg Glu Glu Asp Asp
115 120 125

Phe Ala Val Pro Val Phe Val Asn Ser Arg Arg Phe Gln Ser His Gly
130 135 140

Ser Thr Lys Ser Gly Ile Val Ile Glu Lys His Thr Thr Leu Ala Thr
145 150 155 160

Cys Ser Lys Leu Val Arg Asp Lys Val Lys Met Asn Ala Lys Ser Gly
165 170 175

Gly Phe Ile Asp Leu Ser Ser Thr Glu Glu Val Asp Leu Glu Lys Ser
180 185 190

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Ala Ser Ser Tyr Asp Arg Val Asn Asp Cys Asn Ser Ser Leu Arg Gln
        195                 200                 205

Glu Ser Arg Asn Lys Leu Tyr Arg Asp Gly Gly Glu Ala His Met Lys
    210                 215                 220

Asp Thr Ala Asn Arg Val Glu Ser His Leu Val Thr Glu Ser His Ser
225                 230                 235                 240

Glu Glu Gly His Gly Ser Pro Asp Asp Asp Asp Asn Gly His Glu Tyr
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Cys Arg Ser Arg Gly Gly Val Ser Leu Gln Gln Ile Asn Glu Glu Ala
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Ser Asp Asp Val Ser Asp Asn Ser Met Val Asp Ser Ile Ser Ser Ile
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Asp Val Ser Pro Asp Asp Val Val Gly Ala Leu Gly Gln Lys Arg Phe
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Trp Arg Ala Arg Lys Ala Ile Thr Asn Gln Gln Arg Val Phe Ala Val
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Gln Leu Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg Leu Ile Ala
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Ala Ser Pro Asp Ile Val Leu Asp Glu Ile Asn Tyr Leu Gly Lys Val
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Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Val Pro Ser Glu Phe Ile
        355                 360                 365

Val Lys Pro Pro Leu Pro Gln Val Val Val Asn Lys Gln His Arg Ser
    370                 375                 380

Asp Ser Glu Lys Thr Asp Gln His Lys Met Glu Cys Ser Ala Glu Asn
385                 390                 395                 400

Val Val Gly Arg Leu Ser Asn Gln Gly His His His Asn His Gln Pro
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Ser Asn Tyr Met Pro Phe Pro Ser Asn Pro Pro Ala Ser Pro Ala Val
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420 425 430

Asn Gly Cys Cys Tyr Pro Pro Gln Pro Pro Pro Ser Gly Asn Gln Gln
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Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro
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His Pro Gly Met Gly His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His
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Phe Met Pro Pro Pro Met Val Met Pro Pro Phe His Pro Gly Met Gly
485 490 495

Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Val Ile Pro
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Ala Met Met Asn Pro Tyr Gly Pro Gly Gln Gln Gln Gln Gln Gln Pro
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Gln Ala Asn Glu Gln Thr Asn Gln Phe Gly Tyr Ser Gly Asn Leu Gln
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Asn Asn Thr His Gln Glu Ser Ser Val Asn Glu Ala Ala Pro Pro Gln
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Glu Pro Leu Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln Val
565 570 575

Ser Thr Ala Ser Ser Ala Ser Gly Arg Glu Gly Ile Ser Gly Ser Thr
580 585 590

Ser Phe Arg Pro Phe Ser Ala Val Asp Glu Asp Asn Asn Asp Asn Asn
595 600 605

Asn Asp Ala Pro Asp Gln Met Met Thr Thr Thr Thr Thr Thr Thr Arg
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agcttattgt tacgaaattt tgggtctttt tcaattttag gtcaaataat tggggaaaag 240

ttgagaaatc gtgtgaaatt aggttatttg ggttgagaaa ttttgaagca aagtttgtga 300

gttgtg atg aag aga ggg aaa gat gat gag aag ata ctg gaa cct atg 348
Met Lys Arg Gly Lys Asp Asp Glu Lys Ile Leu Glu Pro Met
1 5 10

ttt cct aga ctt cat gtg aat gat gca gat aaa gga gga cct aga gct 396
Phe Pro Arg Leu His Val Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala
15 20 25 30

cct cct aga aac aag atg gct ctt tat gag cag ctt agt atc cct tct 444
Pro Pro Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser
35 40 45

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gag agg ttt ggt gat cat gga aat ttg tct ctg agt tct cgt agt aac      492
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            50                  55                  60

aac aca agt act ttg gtt cac cct gga cca tct aat cag gtatggagtt      541
Asn Thr Ser Thr Leu Val His Pro Gly Pro Ser Asn Gln
        65                  70                  75

gtggaaattg atgttatata gcttgcaaga gagtagtagg agttgattgt tcaatgtttt    601

cagttgtttt ttagctcatt ttagcttctt ttgttcatgg attgaactca cttgtagata    661

tcggaatata gtggatgtat atctattcta gtgtggaaga ttttttatgt ttgaaagttt    721

tatggatgct tcttgtgatt ggcctgaaca ttctggttac tgtattcaac ttgataagga    781

cattggaaat aatcgttttt ggtgctcttt cctgcag cag tct tgt ggt gtg gaa     836
                                      Gln Ser Cys Gly Val Glu
                                                          80

cga aac tta tct gtc cag cat ctt gat tct tca gct gca gtc cat gta      884
Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Val His Val
            85                  90                  95

act gag aat ttt gtc tcc caa atg ccc ttc atg gaa aat atg aga tct      932
Thr Glu Asn Phe Val Ser Gln Met Pro Phe Met Glu Asn Met Arg Ser
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ttg gca aag cat gat cag agg aaa aca gta aga gag gaa gat gac ttt      980
Leu Ala Lys His Asp Gln Arg Lys Thr Val Arg Glu Glu Asp Asp Phe
    115                 120                 125

gca gtt cca gtg ttt gtt aac tca aga aga ttc cag agt cat ggt agt     1028
Ala Val Pro Val Phe Val Asn Ser Arg Arg Phe Gln Ser His Gly Ser
130                 135                 140                 145

acc aag agt ggg att gtg att gaa aaa cac acg aca ttg gct act tgt     1076
Thr Lys Ser Gly Ile Val Ile Glu Lys His Thr Thr Leu Ala Thr Cys
                150                 155                 160

tca aaa ctt gtt aga gat aag gtg aag atg aac gca aag tca ggt ggc     1124
Ser Lys Leu Val Arg Asp Lys Val Lys Met Asn Ala Lys Ser Gly Gly
            165                 170                 175

ttt ata gat tta tca tca aca gag gaa gtg gat ctc gaa aaa tca gca     1172
Phe Ile Asp Leu Ser Ser Thr Glu Glu Val Asp Leu Glu Lys Ser Ala
        180                 185                 190

tca agt tat gac aga gta aat gat tgt aat tct tcc ttg aga caa gag     1220
Ser Ser Tyr Asp Arg Val Asn Asp Cys Asn Ser Ser Leu Arg Gln Glu
    195                 200                 205

tct aga aat aag tta tac cga gat ggt ggc gaa gct cat atg aag gac     1268
Ser Arg Asn Lys Leu Tyr Arg Asp Gly Gly Glu Ala His Met Lys Asp
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act gct aat aga gtt gaa tct cac ttg gta acg gaa agt cat tct gag     1316
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Thr Ala Asn Arg Val Glu Ser His Leu Val Thr Glu Ser His Ser Glu
                230                 235                 240

gag ggt cat ggc agt cct gat gat gat gac aac ggt cat gaa tac tgc     1364
Glu Gly His Gly Ser Pro Asp Asp Asp Asp Asn Gly His Glu Tyr Cys
            245                 250                 255

aga agc aga gga ggc gtc tct cta cag cag ata aat gaa gak gca agw     1412
Arg Ser Arg Gly Gly Val Ser Leu Gln Gln Ile Asn Glu Xaa Ala Xaa
        260                 265                 270

gat gac rtt tct gat aat tcg atg gtg gat tct ata tcc agc ata gat     1460
Asp Asp Xaa Ser Asp Asn Ser Met Val Asp Ser Ile Ser Ser Ile Asp
    275                 280                 285

gtt tct cct gat gat gtt gtg gga gca tta ggt caa aaa cgt ttc tgg     1508
Val Ser Pro Asp Asp Val Val Gly Ala Leu Gly Gln Lys Arg Phe Trp
290                 295                 300                 305

agg gca agg aag gct att acc aa  gtaagttcac tagtttttt ttacggttta     1561
Arg Ala Arg Lys Ala Ile Thr Asn
                310

gttaactttg ttatttattt tccgctcttt ctatccatct ctttctttga taccgacttt   1621

gctacttgca agaagttaat gctgaagcat agttacctaa ttagactgaa gctttcctct   1681

gctgtttttt ggacactttc ttttagtttc tttgcttttt catgcatact gatacaatgg   1741

atatataact cggtttatat tgtgtctcaa tttgggagaa acgatttcgg gtttttggct   1801

tgagacatga tggtactata gtggagaagc ccccccttga ttcctcgtaa aatggtcctg   1861

ttatatgtta gttgacgagc cctcggtagc atattaacgc gttggatcat gttatagcag   1921

ggagggacat tctctgttga cgtacattgt acaaggtgcc cgccgagaca gttcatggct   1981

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tcttatcgct acgataaggt atcacgatac atgaccaact catataacaa gctttttcta   2341

gcttttcgtt gagggtaagc tagaaatcta ttaacccatc ctttgcttaa cccattcttg   2401

catttaattt ctttttgtgt tattgcttct gttttccctt cgtatttctt cattttacta   2461

ttcgattagc tggtcatatt ccttatgaaa ttccgtttct cattacag t caa caa       2516
                                                      Gln Gln
                                                          315
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aga gta ttt gct gtt caa cta ttt gag ttg cac aga ctg att aag          2561
Arg Val Phe Ala Val Gln Leu Phe Glu Leu His Arg Leu Ile Lys
                320                 325                 330

gtaaagtaat tcagaaaact tctcctataa atatttttgc tgaaacaaac gtcttcatct   2621

gtgctttgtt tctgtaatac tcag gtt caa aga ctt att gct gca tca ccg       2672
                          Val Gln Arg Leu Ile Ala Ala Ser Pro
                                              335

gat atc gtg ctc gac gaa atc aat tac ctt gga aaa gtt tct gct aaa      2720
Asp Ile Val Leu Asp Glu Ile Asn Tyr Leu Gly Lys Val Ser Ala Lys
340                 345                 350                 355

agc tat cca gtg aag aag ctc gtt cca tca gaa ttt atc gta aag cct      2768
Ser Tyr Pro Val Lys Lys Leu Val Pro Ser Glu Phe Ile Val Lys Pro
                360                 365                 370

cct cta cca caa gtt gtc gtc aac aaa cag cac agg agc gac tcc gaa      2816
Pro Leu Pro Gln Val Val Val Asn Lys Gln His Arg Ser Asp Ser Glu
            375                 380                 385

aag act gac caa cat aaa atg gaa tgc tca gct gag aat gtt gtt ggt      2864
Lys Thr Asp Gln His Lys Met Glu Cys Ser Ala Glu Asn Val Val Gly
        390                 395                 400

agg ttg tca aac caa gga cat cat cat aat cat caa cct tcc aac tac      2912
Arg Leu Ser Asn Gln Gly His His His Asn His Gln Pro Ser Asn Tyr
    405                 410                 415

atg cct ttt cca agc aac cca ccc gct tca cca gct gta aac gga tgt      2960
Met Pro Phe Pro Ser Asn Pro Pro Ala Ser Pro Ala Val Asn Gly Cys
420                 425                 430                 435

tgc tat cct cct cag cct cct cct tca gga aac cag caa tgg tta atc      3008
Cys Tyr Pro Pro Gln Pro Pro Pro Ser Gly Asn Gln Gln Trp Leu Ile
                440                 445                 450

cct gtt atg tct cct tct gaa gga ctt ata tac aag cct cat cct ggt      3056
Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro His Pro Gly
            455                 460                 465

atg gga cac acg ggg cac tac gga gga tat tat ggt cat ttt atg cct      3104
Met Gly His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His Phe Met Pro
        470                 475                 480

ccg ccg atg gta atg cct ccg ttt cat ccg ggc atg gga ttc cca cct      3152
Pro Pro Met Val Met Pro Pro Phe His Pro Gly Met Gly Phe Pro Pro
    485                 490                 495

cct ggt aat ggc tac ttc cct cct tat ggt gta atc cca gcc atg atg      3200
Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Val Ile Pro Ala Met Met
500                 505                 510                 515

aac cct tat ggt cca ggc caa caa caa caa caa caa cca caa gcc aat      3248
Asn Pro Tyr Gly Pro Gly Gln Gln Gln Gln Gln Gln Pro Gln Ala Asn
                520                 525                 530
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gaa caa acg aat cag ttt ggg tat tct ggg aat ctt cag aac aac acc     3296
Glu Gln Thr Asn Gln Phe Gly Tyr Ser Gly Asn Leu Gln Asn Asn Thr
            535                 540                 545

cat caa gaa agc tcc gtt aat gaa gct gct cct cca cag gaa cca cta     3344
His Gln Glu Ser Ser Val Asn Glu Ala Ala Pro Pro Gln Glu Pro Leu
        550                 555                 560

aca aag tct tat ccg cgg gct aga aag agc agg caa gtg agc aca gca     3392
Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln Val Ser Thr Ala
    565                 570                 575

agc agt gca agt ggg cga gag gga atc tcc ggt agc act tcc ttt cgt     3440
Ser Ser Ala Ser Gly Arg Glu Gly Ile Ser Gly Ser Thr Ser Phe Arg
580                 585                 590                 595

cca ttc tca gcc gtt gat gag gat aac aac gat aac aac aac gac gca     3488
Pro Phe Ser Ala Val Asp Glu Asp Asn Asn Asp Asn Asn Asn Asp Ala
                600                 605                 610

cct gat caa atg atg aca acc acc acg acc acg aca aga aca act gtt     3536
Pro Asp Gln Met Met Thr Thr Thr Thr Thr Thr Thr Arg Thr Thr Val
            615                 620                 625

act cag aca aca aga gat gga gga gaa gtg acg aga gtg ata aag gtg     3584
Thr Gln Thr Thr Arg Asp Gly Gly Glu Val Thr Arg Val Ile Lys Val
        630                 635                 640

gtt cct cac aat gcg aag ctc gct agt gag a at                       3617
Val Pro His Asn Ala Lys Leu Ala Ser Glu
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Val Gln Gln Leu Ile
5

gcc gga tcg cca gat ctt ttg ttt gat gat ggt gct ttt ctg gga aag 157
Ala Gly Ser Pro Asp Leu Leu Phe Asp Asp Gly Ala Phe Leu Gly Lys
10 15 20 25

tct ctt cca gat gga tct act cct aaa aaa ctc tca ttg gaa tat gtt 205
Ser Leu Pro Asp Gly Ser Thr Pro Lys Lys Leu Ser Leu Glu Tyr Val
30 35 40

gta aaa gct cgg cta caa aat ctt aag cgc aaa gtt gat tct gaa aag 253
Val Lys Ala Arg Leu Gln Asn Leu Lys Arg Lys Val Asp Ser Glu Lys
45 50 55

ata aat caa aac atg gaa tgt tct gca gag aat gct gtt ggt aaa aca 301
Ile Asn Gln Asn Met Glu Cys Ser Ala Glu Asn Ala Val Gly Lys Thr
60 65 70

tct att tcg tcc gtg aaa aat acg agc cac ctt tct agt tcc atg cct 349
Ser Ile Ser Ser Val Lys Asn Thr Ser His Leu Ser Ser Ser Met Pro
75 80 85

ttt gcc gga aat cca cac caa gga aat gtg gca gct gat aat ggg atg 397
Phe Ala Gly Asn Pro His Gln Gly Asn Val Ala Ala Asp Asn Gly Met
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35 40 45

Leu Lys Arg Lys Val Asp Ser Glu Lys Ile Asn Gln Asn Met Glu Cys
50 55 60

Ser Ala Glu Asn Ala Val Gly Lys Thr Ser Ile Ser Ser Val Lys Asn
65 70 75 80

Thr Ser His Leu Ser Ser Ser Met Pro Phe Ala Gly Asn Pro His Gln
85 90 95

Gly Asn Val Ala Ala Asp Asn Gly Met Gly Pro Trp Cys Phe Asn Gln
100 105 110

Ser Pro Gly His
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20 25 30

Glu Asn Gln Lys Pro Val Thr Glu Ala Tyr Pro Glu His Met Lys Pro
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Lys Ile Pro Leu Pro Phe Ile Ser Lys Glu Leu Met Thr Pro Ile Trp
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Gln Gln Gln Leu Leu Pro Pro Gln Glu Asn
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tcctagtgaa atggcacagg gaatcagagc acggaaaatt gctgacggaa gtgatgcacg 420

tctctttctc ttcacgctga tgaaaccaga cagcaaacac aagccatcaa agttgtaccc 480

cataaccgga aatccgcgac ggaatcagca gctagaattg ttcaatccat tcaagaagag 540

agaaaacagc atgat 555

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Ala Ser His Thr Tyr Phe Ala Pro Phe Gly Met Pro Val Met Asn Gln
35 40 45

Ala Thr Ser Gly Ser Ala Val Glu Gln Val Asn Gln Phe Ala Ala Gln
50 55 60

Gly Ser His Gly Gln Asn Gly His Ser Ser Val Glu Gly Ala Asp Phe
65 70 75 80

Asn Thr His His Asn Gln Ser Ser Ser Asn Leu Pro Val Gln Lys Asn
85 90 95

Gly Ala Arg Leu His Val Lys Lys Ser Gln Ala Leu Lys Glu Arg Gly
100 105 110

Leu Gln Gly Ser Thr Arg Ser Ser Pro Ser Glu Met Ala Gln Gly Ile
115 120 125

Arg Ala Arg Lys Ile Ala Asp Gly Ser Asp Ala Gln Ser Leu Ser Leu

130 135 140

His Ala Asp Glu Thr Arg Gln Gln Thr Gln Ala Ile Lys Val Val Pro
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His Asn Arg Lys Ser Ala Thr Glu Ser Ala Ala Arg Ile Val Gln Ser
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Ile Gln Glu Glu Arg Lys Gln His Asp
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aaatataata gtaattttgt gaaattatac atctttttg cttctgtgtg cttcagaaat 180

ctcttgattt ctatgtaaag attgtgtttt gggtatttgg gtcggtagaa ttcttgtttt 240

tttaggtggg gtttgcttgg ttttcttcaa ttttgattgg ttttgttgaa aagttcagaa 300

atttgatgta attgtacgga tttctttgaa ttttggaagt tgaatgtatg gtaaagtttc 360

gtttttttgg tttaatttaa tgaatgttgg agattgggtg aacctgttga gaagctatta 420

aagggaagaa atgaagagag gaaagggtga agagaagttg atgggaccta tgtttccaag 480

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Thr Gly Glu Glu Lys Val Met Gly Pro Met Phe Pro Arg Leu Asn Val
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aat gat aca gaa aaa gga ggt cca aga gca cct cca agg aac aag atg 151
Asn Asp Thr Glu Lys Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met
25 30 35

gct ctt tat gaa caa ctg agt atc cct tcc caa cga tac aac cct ggt 199
Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg Tyr Asn Pro Gly
40 45 50

gat ttg cct cat aac agt agt aac agt gca aat ttg gtc ctt cct cac 247
Asp Leu Pro His Asn Ser Ser Asn Ser Ala Asn Leu Val Leu Pro His
55 60 65

cca agc cag gag aat gaa cac gaa aga ggt gta tta ttc tct aga caa 295
Pro Ser Gln Glu Asn Glu His Glu Arg Gly Val Leu Phe Ser Arg Gln
70 75 80

ctt cct gca tta aga cat cca gtt gaa aag cca tat gga cgt agt tct 343
Leu Pro Ala Leu Arg His Pro Val Glu Lys Pro Tyr Gly Arg Ser Ser
85 90 95 100

ggt tca aat act cca ttg cgg gaa gtt aag tct aaa agg cag aca gaa 391
Gly Ser Asn Thr Pro Leu Arg Glu Val Lys Ser Lys Arg Gln Thr Glu
105 110 115

aag gaa gat ttt aga gtt ccc act ttt gat aac tcc aag gag cgt gca 439
Lys Glu Asp Phe Arg Val Pro Thr Phe Asp Asn Ser Lys Glu Arg Ala
120 125 130

gta aac aca gag gac tat tct aaa ggt acc tca gat ata gat aag cga 487
Val Asn Thr Glu Asp Tyr Ser Lys Gly Thr Ser Asp Ile Asp Lys Arg
135 140 145

gac agt act ttg aag cgg act gat caa ctc tcc cat gtc aca ccg aga 535
Asp Ser Thr Leu Lys Arg Thr Asp Gln Leu Ser His Val Thr Pro Arg
150 155 160

gag aat ctt gtt aat acc ttt ggt gaa tca cat aag acc aat ata gt 582
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tct gga aca gac atc tct cct gat gac att gta gga ata att ggc tta      97
Ser Gly Thr Asp Ile Ser Pro Asp Asp Ile Val Gly Ile Ile Gly Leu
            20                  25                  30

aag cgt ttc tgg aaa gcc aga aga gca att gtc aac cag caa aga gtg     145
Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
        35                  40                  45

ttt gca atc caa gtg ttc gag ttg cat cga cta ata aag gta caa agg     193
Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg
    50                  55                  60

ctc att gcc ggg tca cca aat agt tcg ctc gaa gat cct gct tat tta     241
Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala Tyr Leu
65                  70                  75                  80

ggc aaa cct tta aag agt tca tcg atc aaa aga ctt cca ttg gac tgt     289
Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu Asp Cys
                85                  90                  95

att gtt aga gaa tct caa agt gtt ctg aag cgc aag cat gat tct gag     337
Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp Ser Glu
            100                 105                 110

aag cct cac ttc agg atg gaa cac act gcc gaa agc aat gtg gga aag     385
Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val Gly Lys
        115                 120                 125

gca tct ctc tct act gtg caa aat ggt agt caa ctc tct agc cac aaa     433
Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser His Lys
    130                 135                 140

cca ttt tca gga act cca ctg cct aca cct gta aca aat gat tct aat     481
Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp Ser Asn
145                 150                 155                 160

gcg ggt cct tgg tgc ttc caa caa cct tcc ggg cac caa tgg ttg atc     529
Ala Gly Pro Trp Cys Phe Gln Gln Pro Ser Gly His Gln Trp Leu Ile
                165                 170                 175
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cca gtg atg tct cct tct gag gga ctt gta tac aag cca ttt tct gga      577
Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe Ser Gly
            180                 185                 190

cct gga ttc acg agt cct att tgt gga agt ggg cct tca gga tcg agt      625
Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Ser Gly Ser Ser
        195                 200                 205

cca aca atg ggg aac ttt ttt gct cca aca tat gga gtt cct gct cct      673
Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro Ala Pro
    210                 215                 220

aat cct cac tat caa ggt atg gga gtt cct ttt gca cct ccg act ggt      721
Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro Thr Gly
225                 230                 235                 240

cat ggt tac ttt cgg caa tat ggc atg cca gct atg aat cca cca att      769
His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro Pro Ile
                245                 250                 255

tca tca act gct agt gaa gaa tcg aac cag tat acc atg cct ggt tta      817
Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro Gly Leu
            260                 265                 270

caa cac cag ttt tct gga gta gtt gat gac gtt caa cat tca aca tca      865
Gln His Gln Phe Ser Gly Val Val Asp Asp Val Gln His Ser Thr Ser
        275                 280                 285

gga ctc agt aat gtt cta aat cag aag aaa gaa aat gtc ccg gat gtt      913
Gly Leu Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro Asp Val
    290                 295                 300

gta agg tat caa tcc aca aaa gat aat gag gta caa gcc agc agt gca      961
Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser Ser Ala
305                 310                 315                 320

agt agt cct att gag aca gca gga aga aac atg ctc tct ctt ttt ccc     1009
Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu Phe Pro
                325                 330                 335

acg tct cca gtt act gac aac cgt gat ggt agc cct cag gct tgt gtg     1057
Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala Cys Val
            340                 345                 350

cct gat aat cca gcc aga gtt atc aag gtt gta cct cac aat gca agg     1105
Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn Ala Arg
        355                 360                 365

tct gct aca gaa tcc gta gct cgg ata ttt cag tct ata caa caa gag     1153
Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile Gln Gln Glu
    370                 375                 380

aga aat aat atg act tag gtttaacaca tctataagta gcttaccttg            1201
Arg Asn Asn Met Thr
385

tgaatatgac catttgctca tcctggcaaa atgtagtagt ttcagtcaat ttgttgtatc   1261
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tttcttttct acagaaagta tgtaatagct gtattttaat ttggttgctg tagataagca 1321

tacctgcaaa aaaaaaaaaa aaaaac 1347

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<213> Lycopersicon esculentum

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1 5 10 15

Ser Gly Thr Asp Ile Ser Pro Asp Asp Ile Val Gly Ile Ile Gly Leu
20 25 30

Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
35 40 45

Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Arg
50 55 60

Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala Tyr Leu
65 70 75 80

Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu Asp Cys
85 90 95

Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp Ser Glu
100 105 110

Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val Gly Lys
115 120 125

Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser His Lys
130 135 140

Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp Ser Asn
145 150 155 160

Ala Gly Pro Trp Cys Phe Gln Gln Pro Ser Gly His Gln Trp Leu Ile
165 170 175

Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe Ser Gly
180 185 190

Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Ser Gly Ser Ser
195 200 205

Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro Ala Pro
210 215 220

Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro Thr Gly
225 230 235 240

His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro Pro Ile
245 250 255

Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro Gly Leu
260 265 270

Gln His Gln Phe Ser Gly Val Val Asp Asp Val Gln His Ser Thr Ser
275 280 285

Gly Leu Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro Asp Val
290 295 300

Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser Ser Ala
305 310 315 320

Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu Phe Pro
325 330 335

Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala Cys Val
340 345 350

Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn Ala Arg
355 360 365

Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile Gln Gln Glu
370 375 380

Arg Asn Asn Met Thr
385

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Arg Leu Asn Val Asn Asp Thr Glu Lys Gly Gly Pro Arg Ala Pro Pro
20 25 30

Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
35 40 45

Tyr Asn Pro Gly Asp Leu Pro His Asn Ser Ser Asn Ser Ala Asn Leu
50 55 60

Val Leu Pro His Pro Ser Gln Glu Asn Glu His Glu Arg Gly Val Leu
65 70 75 80

Phe Ser Arg Gln Leu Pro Ala Leu Arg His Pro Val Glu Lys Pro Tyr
85 90 95

Gly Arg Ser Ser Gly Ser Asn Thr Pro Leu Arg Glu Val Lys Ser Lys
100 105 110

Arg Gln Thr Glu Lys Glu Asp Phe Arg Val Pro Thr Phe Asp Asn Ser
115 120 125

Lys Glu Arg Ala Val Asn Thr Glu Asp Tyr Ser Lys Gly Thr Ser Asp
130 135 140

Ile Asp Lys Arg Asp Ser Thr Leu Lys Arg Thr Asp Gln Leu Ser His
145 150 155 160

Val Thr Pro Arg Glu Asn Leu Val Asn Thr Phe Gly Glu Ser His Lys
165 170 175

Thr Asn Ile

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1 5 10 15

Arg Leu His Val Asn Asp Thr Glu Lys Gly Gly Pro Lys Ala Pro Pro
20 25 30

Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
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Met Ala Thr Arg Gly Gly Gly Gly Gly Gly Gly Gly Lys Glu Ala Lys
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Gly Lys Val Met Gly Pro Leu Phe Pro Arg Leu His Val Asn Asp Ala
20 25 30

gcc aag ggc gga ggc ccg cgg gcg ccg ccc cgg aac aag atg gcg ctc 144
Ala Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu
35 40 45

tac gag cag ttc acc gtg ccc tcg cat cgc ttc agc ggc gga gga ggc 192
Tyr Glu Gln Phe Thr Val Pro Ser His Arg Phe Ser Gly Gly Gly Gly
50 55 60

ggc ggc gga gta gga ggc agc ccc gcg cac tcg acg tcg gcg gcg agc 240
Gly Gly Gly Val Gly Gly Ser Pro Ala His Ser Thr Ser Ala Ala Ser
65 70 75 80

cag agc cag agc cag agc cag gtgactcgac gtcctgcccg tatgatcgat 291
Gln Ser Gln Ser Gln Ser Gln
85

tcgattgggg gtagtgtgtg cgactgctaa attggtacta gtaggcgaca attctgtgca 351

aatggagcta aacgccttgc aaatcgaatc gaattagaag cctaaattgg taggcaataa 411

ttctgtgcaa tggagctaaa cttccttgca aatcgaatag aactaaaagc tgggaagata 471

atttcgaggc acaaatggtg ccctcgacgt cgacgagcta ggtcagaggg ggcgtttcac 531

gccttaccct ttgtagttat ctcggttggg atagatgaat tgatgggcga atttagtgca 591

acggagctaa acacatggaa aaattggata agattaaggc cgagaagccc agtttgaggc 651

acaaatgcca tgttcctttt gtgctgatta atctatcatg ccgtcgacat gtgattcaat 711

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gtcattattg atctttctcc gtgctgataa ctcacttgtg ttgaaggcga aagagcagaa 831

caaaaccatt atatgcagtt tacatcagct cttccggtaa agttttggag acggggcata 891

agttccttgc aaacaatatc ggatattata gcttattgca aattgtatat ggccagatat 951

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gctatgattg tgtttgctga ggtctggtgt ttgtaatata caaacaaaaa ggtccacatg   1011

tgaaactgca tgtagcgcag gtggcaaaga gtagccgtag tgctgctcaa cgtactgtgt   1071

tctattctcc ctgacgtgct caccttcctt aaatcattga cactaggttc ctccttagtg   1131

tcttgcattt ttgcctgccg aaaaaaaaag gtccacgtga aagggaatga taaaaatggt   1191

ggttgatatg ctttgattgt caggcacacg ttcaacctgt atgtgataaa tatcaacggt   1251

tttctaatac tgttttcagc aaggatttag gagtggaaaa tattctttag aacaaatctg   1311

caatagcctc ccacaacaca tccaactacc ttttgataat gggatagtta tagacatgaa   1371

gtgcgaatgg caaaagtcca agtcatagat ttccaaatga agaaatgtga acaaaataag   1431

aaagaaagaa gtccatttgc agtattatgt ctcttttgcc cttctttggg tcgaaaataa   1491

aataaaaaat cgagatctta ccatgagata cttaatctcc caccactttt tctaattcaa   1551

catggaagtt cttggatagt ttaaatacgc ttcctaccaa ttagcgtgga atcctcgcaa   1611

ttttttcacta aatctagtag tactgaaatg gattttattt tcttccag gtt tat gga   1668
                                                    Val Tyr Gly
                                                                90

cgt gac agt tct ctg ttc cag ccg ttc aat gtg cct tcc aat cga cct     1716
Arg Asp Ser Ser Leu Phe Gln Pro Phe Asn Val Pro Ser Asn Arg Pro
                95                  100                 105

ggc cat tct act gaa aag atc aat tca gat aag atc aac aag aag att     1764
Gly His Ser Thr Glu Lys Ile Asn Ser Asp Lys Ile Asn Lys Lys Ile
            110                 115                 120

agt ggt tca aga aaa gaa ctg ggg atg tta tcc tct cag act aag ggc     1812
Ser Gly Ser Arg Lys Glu Leu Gly Met Leu Ser Ser Gln Thr Lys Gly
        125                 130                 135

atg gat att tat gct tca aga tca act gct gag gca cca caa aga aga     1860
Met Asp Ile Tyr Ala Ser Arg Ser Thr Ala Glu Ala Pro Gln Arg Arg
    140                 145                 150

gca gaa aat aca ata aag agt tct tcg gga aag aga ttg gcc gat gat     1908
Ala Glu Asn Thr Ile Lys Ser Ser Ser Gly Lys Arg Leu Ala Asp Asp
155                 160                 165                 170

gat gaa ttt atg gtt cct tct gtc ttc aat tcc aga ttt cct caa tat     1956
Asp Glu Phe Met Val Pro Ser Val Phe Asn Ser Arg Phe Pro Gln Tyr
                175                 180                 185

agt act caa gag aat gca ggg gtt caa gac caa tca aca ccc ctt gtt     2004
Ser Thr Gln Glu Asn Ala Gly Val Gln Asp Gln Ser Thr Pro Leu Val
            190                 195                 200

gct gca aat cca cac aaa agc cct tca aca gtg tcc aaa tca tcc aca     2052
Ala Ala Asn Pro His Lys Ser Pro Ser Thr Val Ser Lys Ser Ser Thr
        205                 210                 215
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aag tgt tat aac act gtt agc aag aaa ttg gag aga atc cat gtt tct     2100
Lys Cys Tyr Asn Thr Val Ser Lys Lys Leu Glu Arg Ile His Val Ser
    220                 225                 230

gat gtg aaa tca agg acc cct ttg aaa gac aag gag atg gaa gca gca     2148
Asp Val Lys Ser Arg Thr Pro Leu Lys Asp Lys Glu Met Glu Ala Ala
235                 240                 245                 250

cag aca tcc aaa aac gtg gaa gtt gaa aaa agt tca tcc ttt cat gct     2196
Gln Thr Ser Lys Asn Val Glu Val Glu Lys Ser Ser Ser Phe His Ala
                255                 260                 265

tcc aaa gat atg ttt gaa agc agg cat gct aaa gta tat cct aag atg     2244
Ser Lys Asp Met Phe Glu Ser Arg His Ala Lys Val Tyr Pro Lys Met
            270                 275                 280

gat aag acg ggc att ata aat gat tct gat gag cca cat ggt gga aat     2292
Asp Lys Thr Gly Ile Ile Asn Asp Ser Asp Glu Pro His Gly Gly Asn
        285                 290                 295

agt ggg cat caa gcg aca agc aga aat gga ggt tcc atg aaa ttt cag     2340
Ser Gly His Gln Ala Thr Ser Arg Asn Gly Gly Ser Met Lys Phe Gln
    300                 305                 310

aac cct cca atg aga aga aat gaa att tcc tct aat cca tct tct gaa     2388
Asn Pro Pro Met Arg Arg Asn Glu Ile Ser Ser Asn Pro Ser Ser Glu
315                 320                 325                 330

aat act gat agg cat tat aat tta ccg caa gga ggc ata gag gaa aca     2436
Asn Thr Asp Arg His Tyr Asn Leu Pro Gln Gly Gly Ile Glu Glu Thr
                335                 340                 345

ggt aca aag aga aaa agg ttg cta gaa caa cac gat gca gag aaa agt     2484
Gly Thr Lys Arg Lys Arg Leu Leu Glu Gln His Asp Ala Glu Lys Ser
            350                 355                 360

gat gat gtg tca agg ttg cta gaa caa cac gat gca gag aac att gat     2532
Asp Asp Val Ser Arg Leu Leu Glu Gln His Asp Ala Glu Asn Ile Asp
        365                 370                 375

gat gtg tct gat tcc tcg gtg gag tgt ata act ggt tgg gag att tct     2580
Asp Val Ser Asp Ser Ser Val Glu Cys Ile Thr Gly Trp Glu Ile Ser
    380                 385                 390

cca gat aaa att gtt gga gcc att ggt aca aag cat ttc tgg aaa gca     2628
Pro Asp Lys Ile Val Gly Ala Ile Gly Thr Lys His Phe Trp Lys Ala
395                 400                 405                 410

aga cgt gct att atg aa  gtaagtaaaa ctatcctttt gagcttagtt           2675
Arg Arg Ala Ile Met Asn
                415

tggcccactc aaactagact tgtttgcagc tctaattacg tataggtagc tttgatgaat   2735

aaaatttgtt ttgtttccct tgctttactg ttatttgctc ttaatttgcg gttgatctta   2795
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atcatcttag acagaaaaac atgatgacta tctcgtttgt ttttggttta tttcatattt   2855

gaatgccaat agatgtcagc tccagatgat atttcaaata cctcatgcat ggaaactgtg   2915

catacttatg ccaaattttg ggcttacaag tcagcatgtc tacaaatttc tttggcagaa   2975

ttaatatata tctagttcaa catttgctga tttgtaattg gattagttgt ctgcagaatg   3035

ccggcatgtt ttattttcct ttcaactagg tcaatcagtt ttgttgttgt ctgttgttct   3095

tgtccaccta cacctgtact actgaaatgt tctcttttgg agatgtcaat gaaaatttta   3155

atctatagtg gtttcaattt tattttcatt ttagtcaaga agaatggcat aatctcattt   3215

aaaaagattg taaaagtgtc cctgttaaag tgatattgta ggtattgctt taccaagcta   3275

ctgtatgatt ccctttattg ttttacactc taatcttctt taaactctat gcag t caa   3333
                                                              Gln

cag agg gtg ttt gct gtc cag gtt ttt gag ctg cat aag ttg gta aaa     3381
Gln Arg Val Phe Ala Val Gln Val Phe Glu Leu His Lys Leu Val Lys
        420                 425                 430

gtgagtctag caaatttctc ttccttctag ccactcttaa gcaggttaat tcgtggatag   3441

gattttgtcc ataatctgtt tataacccac acttgtattt gacttacaat cag gtg      3497
                                                            Val

cag aag ttg att gca gca tcg cca cat gta ctt att gaa agt gat cct     3545
Gln Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Ser Asp Pro
435                 440                 445                 450

tgc ctt ggc aat gcc ttg ttg ggt agc aag aac aag ctg gtg gaa gaa     3593
Cys Leu Gly Asn Ala Leu Leu Gly Ser Lys Asn Lys Leu Val Glu Glu
                455                 460                 465

aac ctg aaa gca caa cct ctt tta gtc gca acc atc gat gac gtg gag     3641
Asn Leu Lys Ala Gln Pro Leu Leu Val Ala Thr Ile Asp Asp Val Glu
            470                 475                 480

cca agt cta cag caa ccg gag gta tca aaa gaa aac act gaa gac agc     3689
Pro Ser Leu Gln Gln Pro Glu Val Ser Lys Glu Asn Thr Glu Asp Ser
        485                 490                 495

cca ccc tcc cct cat gat act ggg ctt ggc agt ggt caa cgt gat caa     3737
Pro Pro Ser Pro His Asp Thr Gly Leu Gly Ser Gly Gln Arg Asp Gln
    500                 505                 510

gct gca aca aat ggc gtc tct aaa agc aat cgt cga gct aca cct gtt     3785
Ala Ala Thr Asn Gly Val Ser Lys Ser Asn Arg Arg Ala Thr Pro Val
515                 520                 525                 530

gct tct gat aac aaa caa aat aac tgg ggc gtt caa ctt caa cca cct     3833
Ala Ser Asp Asn Lys Gln Asn Asn Trp Gly Val Gln Leu Gln Pro Pro
                535                 540                 545
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caa aat caa tgg ctt gtc cct gtc atg tct cct ttg gaa ggc ctt gtc     3881
Gln Asn Gln Trp Leu Val Pro Val Met Ser Pro Leu Glu Gly Leu Val
            550                 555                 560

tat aag cct tat tct ggt ccg tgc cct cca gct ggt agc ata ttg gcc     3929
Tyr Lys Pro Tyr Ser Gly Pro Cys Pro Pro Ala Gly Ser Ile Leu Ala
        565                 570                 575

ccg ttt tat gcc aac tgt act cct ttg agt ctt cca tca aca gct gga     3977
Pro Phe Tyr Ala Asn Cys Thr Pro Leu Ser Leu Pro Ser Thr Ala Gly
    580                 585                 590

gat ttc atg aac tcg gca tac ggt gtt cct atg cct cat cag cca caa     4025
Asp Phe Met Asn Ser Ala Tyr Gly Val Pro Met Pro His Gln Pro Gln
595                 600                 605                 610

cat atg ggt gct cct ggc cct cct tcc atg cct atg aac tac ttc ccg     4073
His Met Gly Ala Pro Gly Pro Pro Ser Met Pro Met Asn Tyr Phe Pro
                615                 620                 625

cct ttc agc ata cca gtg atg aac cca act gca ccg gca cct gta gtc     4121
Pro Phe Ser Ile Pro Val Met Asn Pro Thr Ala Pro Ala Pro Val Val
            630                 635                 640

gaa caa ggg aga cat cct tcg atg cca cag cct tat ggg aac ttt gag     4169
Glu Gln Gly Arg His Pro Ser Met Pro Gln Pro Tyr Gly Asn Phe Glu
        645                 650                 655

cag cag tcg tgg atc tca tgt aac atg tca cat cca agt ggc att tgg     4217
Gln Gln Ser Trp Ile Ser Cys Asn Met Ser His Pro Ser Gly Ile Trp
    660                 665                 670

aga ttt cat gcc tca aga gat agc gag gca cag gcc agc agc gct agc     4265
Arg Phe His Ala Ser Arg Asp Ser Glu Ala Gln Ala Ser Ser Ala Ser
675                 680                 685                 690

agt cct ttt gac agg ttc caa tgc agt gga agt ggt cct gta tcc gcc     4313
Ser Pro Phe Asp Arg Phe Gln Cys Ser Gly Ser Gly Pro Val Ser Ala
                695                 700                 705

ttc ccc aca gta tca gct cag aac aac cag cct cag ccc tca tat agc     4361
Phe Pro Thr Val Ser Ala Gln Asn Asn Gln Pro Gln Pro Ser Tyr Ser
            710                 715                 720

agc cgg gac aac cag acc aat gtt atc aag gtt gtt cca cat aat tca     4409
Ser Arg Asp Asn Gln Thr Asn Val Ile Lys Val Val Pro His Asn Ser
        725                 730                 735

cga act gct tca gag tca gca gca cgg att ttc cgg tca ata caa atg     4457
Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Ser Ile Gln Met
    740                 745                 750

gaa cgg caa cga gat gat tga                                        4478
Glu Arg Gln Arg Asp Asp
755                 760
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Ala Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu
35 40 45

Tyr Glu Gln Phe Thr Val Pro Ser His Arg Phe Ser Gly Gly Gly Gly
50 55 60

Gly Gly Gly Val Gly Gly Ser Pro Ala His Ser Thr Ser Ala Ala Ser
65 70 75 80

Gln Ser Gln Ser Gln Ser Gln Val Tyr Gly Arg Asp Ser Ser Leu Phe
85 90 95

Gln Pro Phe Asn Val Pro Ser Asn Arg Pro Gly His Ser Thr Glu Lys
100 105 110

Ile Asn Ser Asp Lys Ile Asn Lys Lys Ile Ser Gly Ser Arg Lys Glu
115 120 125

Leu Gly Met Leu Ser Ser Gln Thr Lys Gly Met Asp Ile Tyr Ala Ser
130 135 140

Arg Ser Thr Ala Glu Ala Pro Gln Arg Arg Ala Glu Asn Thr Ile Lys
145 150 155 160

Ser Ser Ser Gly Lys Arg Leu Ala Asp Asp Asp Glu Phe Met Val Pro
165 170 175

Ser Val Phe Asn Ser Arg Phe Pro Gln Tyr Ser Thr Gln Glu Asn Ala
180 185 190

Gly Val Gln Asp Gln Ser Thr Pro Leu Val Ala Ala Asn Pro His Lys

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        195                 200                 205

Ser Pro Ser Thr Val Ser Lys Ser Ser Thr Lys Cys Tyr Asn Thr Val
    210                 215                 220

Ser Lys Lys Leu Glu Arg Ile His Val Ser Asp Val Lys Ser Arg Thr
225                 230                 235                 240

Pro Leu Lys Asp Lys Glu Met Glu Ala Ala Gln Thr Ser Lys Asn Val
                245                 250                 255

Glu Val Glu Lys Ser Ser Ser Phe His Ala Ser Lys Asp Met Phe Glu
            260                 265                 270

Ser Arg His Ala Lys Val Tyr Pro Lys Met Asp Lys Thr Gly Ile Ile
        275                 280                 285

Asn Asp Ser Asp Glu Pro His Gly Gly Asn Ser Gly His Gln Ala Thr
    290                 295                 300

Ser Arg Asn Gly Gly Ser Met Lys Phe Gln Asn Pro Pro Met Arg Arg
305                 310                 315                 320

Asn Glu Ile Ser Ser Asn Pro Ser Ser Glu Asn Thr Asp Arg His Tyr
                325                 330                 335

Asn Leu Pro Gln Gly Gly Ile Glu Glu Thr Gly Thr Lys Arg Lys Arg
            340                 345                 350

Leu Leu Glu Gln His Asp Ala Glu Lys Ser Asp Asp Val Ser Arg Leu
        355                 360                 365

Leu Glu Gln His Asp Ala Glu Asn Ile Asp Asp Val Ser Asp Ser Ser
    370                 375                 380

Val Glu Cys Ile Thr Gly Trp Glu Ile Ser Pro Asp Lys Ile Val Gly
385                 390                 395                 400

Ala Ile Gly Thr Lys His Phe Trp Lys Ala Arg Arg Ala Ile Met Asn
                405                 410                 415

Gln Gln Arg Val Phe Ala Val Gln Val Phe Glu Leu His Lys Leu Val
            420                 425                 430
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Lys Val Gln Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Ser
        435                 440                 445

Asp Pro Cys Leu Gly Asn Ala Leu Leu Gly Ser Lys Asn Lys Leu Val
    450                 455                 460

Glu Glu Asn Leu Lys Ala Gln Pro Leu Leu Val Ala Thr Ile Asp Asp
465                 470                 475                 480

Val Glu Pro Ser Leu Gln Gln Pro Glu Val Ser Lys Glu Asn Thr Glu
                485                 490                 495

Asp Ser Pro Pro Ser Pro His Asp Thr Gly Leu Gly Ser Gly Gln Arg
            500                 505                 510

Asp Gln Ala Ala Thr Asn Gly Val Ser Lys Ser Asn Arg Arg Ala Thr
        515                 520                 525

Pro Val Ala Ser Asp Asn Lys Gln Asn Asn Trp Gly Val Gln Leu Gln
    530                 535                 540

Pro Pro Gln Asn Gln Trp Leu Val Pro Val Met Ser Pro Leu Glu Gly
545                 550                 555                 560

Leu Val Tyr Lys Pro Tyr Ser Gly Pro Cys Pro Pro Ala Gly Ser Ile
                565                 570                 575

Leu Ala Pro Phe Tyr Ala Asn Cys Thr Pro Leu Ser Leu Pro Ser Thr
            580                 585                 590

Ala Gly Asp Phe Met Asn Ser Ala Tyr Gly Val Pro Met Pro His Gln
        595                 600                 605

Pro Gln His Met Gly Ala Pro Gly Pro Pro Ser Met Pro Met Asn Tyr
    610                 615                 620

Phe Pro Pro Phe Ser Ile Pro Val Met Asn Pro Thr Ala Pro Ala Pro
625                 630                 635                 640

Val Val Glu Gln Gly Arg His Pro Ser Met Pro Gln Pro Tyr Gly Asn
                645                 650                 655
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Phe Glu Gln Gln Ser Trp Ile Ser Cys Asn Met Ser His Pro Ser Gly
            660                 665                 670

Ile Trp Arg Phe His Ala Ser Arg Asp Ser Glu Ala Gln Ala Ser Ser
        675                 680                 685

Ala Ser Ser Pro Phe Asp Arg Phe Gln Cys Ser Gly Ser Gly Pro Val
    690                 695                 700

Ser Ala Phe Pro Thr Val Ser Ala Gln Asn Asn Gln Pro Gln Pro Ser
705                 710                 715                 720

Tyr Ser Ser Arg Asp Asn Gln Thr Asn Val Ile Lys Val Val Pro His
                725                 730                 735

Asn Ser Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Ser Ile
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Gln Met Glu Arg Gln Arg Asp Asp
        755                 760
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gctattgtca atcagcagag ggtatttgct gttcaagtat tcgagctgca taggttgatc 180

aaagtgcaga agttgatcgc tgcatctcca catgtactta ttgaggggga tccttgcctt 240

ggcaaatcct tggcggtgag cmagaaaagg ctgaagtcag tggctgattc ccgtwatgtc 300

cccgtttgaa ggacttgtct acaagcctta tcccgggsca ytgccctccg gtggaagtct 360

tttggcgccc ccatttttg ccagctaccc cacctcttcc tcctccacag ctgggggga 420

tttcatgagt tcggcatgtg gagccaggct gatgagtgcc cctgtgtact tcccgtcttt 480

cagcatgcct gcagtgtcag ggtctgcagt tgagcaagtg agccatgttg cagcgtcgca 540

gcataaacgg aactcgtgta gtgaagcggt gttggcatca agggacagcg aggtgcaagg 600

cagtagtgct agcagtccgg catcttctga aacagcagct caacccaggg tcattagggt 660

tgttccccac acggcacgca cggcttcaga gtcggcagca aggattttcc gctcaataca 720

gatggagagg aaacaaaacg acccgtgact ggcagataaa aatgaaagaa cggagggagt 780

agactaattt tttgaccgat aattataatg atcgccgtaa attggctggc ccgcccgcct 840

tatgtttttt gttcagtgta aatatgctgt gtctgtcaga atgatatggc atctgtagct 900

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Asp Val Glu Gln Asn Asp Asp Leu Ser Asp Ser Ser Val Glu Ser Leu
1 5 10 15

Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly Pro
20 25 30

Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
35 40 45

Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Lys
50 55 60

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Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys Leu
65                  70                  75                  80

Gly Lys Ser Leu Ala Val Ser Xaa Lys Arg Leu Ser Gln Trp Leu Ile
                85                  90                  95

Pro Xaa Met Ser Pro Phe Glu Gly Leu Val Tyr Lys Pro Tyr Pro Gly
            100                 105                 110

Xaa Xaa Pro Ser Gly Gly Ser Leu Leu Ala Pro Pro Phe Phe Ala Ser
        115                 120                 125

Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly Gly Asp Phe Met Ser Ser
    130                 135                 140

Ala Cys Gly Ala Arg Leu Met Ser Ala Pro Val Tyr Phe Pro Ser Phe
145                 150                 155                 160

Ser Met Pro Ala Val Ser Gly Ser Ala Val Glu Gln Val Ser His Val
                165                 170                 175

Ala Ala Ser Gln His Lys Arg Asn Ser Cys Ser Glu Ala Val Leu Ala
            180                 185                 190

Ser Arg Asp Ser Glu Val Gln Gly Ser Ser Ala Ser Ser Pro Ala Ser
        195                 200                 205

Ser Glu Thr Ala Ala Gln Pro Arg Val Ile Arg Val Val Pro His Thr
    210                 215                 220

Ala Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Ser Ile Gln
225                 230                 235                 240

Met Glu Arg Lys Gln Asn Asp Pro
                245
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Ala Arg Gly His Met Val Pro Pro Gly Ala Pro Ala Met His Met Asn
1               5                   10                  15

tac ttc ccg cct ttc agt atg cca gtg atg aat cca gga aca cca gca       96
Tyr Phe Pro Pro Phe Ser Met Pro Val Met Asn Pro Gly Thr Pro Ala
            20                  25                  30

tct gca gtg gag caa ggg agc cat gct gct gcg cca cag cct cat ggg      144
Ser Ala Val Glu Gln Gly Ser His Ala Ala Ala Pro Gln Pro His Gly
        35                  40                  45

cac atg gac cag cag tcg ctg atc tca tgt aac atg tca cac ccg agt      192
His Met Asp Gln Gln Ser Leu Ile Ser Cys Asn Met Ser His Pro Ser
    50                  55                  60

ggc gtt tgg agg ttt ctt gca tca agg gac agc gag cca cag gcc agc      240
Gly Val Trp Arg Phe Leu Ala Ser Arg Asp Ser Glu Pro Gln Ala Ser
65                  70                  75                  80

agc gcc acc agc cct ttc gac agg ctc caa gtc caa ggt gat gga agt      288
Ser Ala Thr Ser Pro Phe Asp Arg Leu Gln Val Gln Gly Asp Gly Ser
                85                  90                  95

gct ccg ttg tca ttc ttt ccc acg gct tca gct ccg aat gtc cag cct      336
Ala Pro Leu Ser Phe Phe Pro Thr Ala Ser Ala Pro Asn Val Gln Pro
            100                 105                 110

ccg ccc tca tct gga ggc cgg gac cgg gac cag cag aac cat gta atc      384
Pro Pro Ser Ser Gly Gly Arg Asp Arg Asp Gln Gln Asn His Val Ile
        115                 120                 125

agg gtt gtt ccg cgt aac gca cag act gct tca gtc ccg aaa gcc caa      432
Arg Val Val Pro Arg Asn Ala Gln Thr Ala Ser Val Pro Lys Ala Gln
    130                 135                 140

cct cag ccg tca tcc gga ggc cgg gac caa aag aac cat gta atc agg      480
Pro Gln Pro Ser Ser Gly Gly Arg Asp Gln Lys Asn His Val Ile Arg
145                 150                 155                 160

gtt gtt ccg cat aac gcg cag act gct tcg gag tca gca gcg tgg atc      528
Val Val Pro His Asn Ala Gln Thr Ala Ser Glu Ser Ala Ala Trp Ile
                165                 170                 175

ttc cgg tca ata caa atg gag agg aac caa aat gat tcg tag              570
Phe Arg Ser Ile Gln Met Glu Arg Asn Gln Asn Asp Ser
            180                 185
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ctggttacca tatactttcg tgtcatccga tggcagctta gtgcagcatt gcagt 625

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<213> Zea mays

<400> 31

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Tyr Phe Pro Pro Phe Ser Met Pro Val Met Asn Pro Gly Thr Pro Ala
20 25 30

Ser Ala Val Glu Gln Gly Ser His Ala Ala Ala Pro Gln Pro His Gly
35 40 45

His Met Asp Gln Gln Ser Leu Ile Ser Cys Asn Met Ser His Pro Ser
50 55 60

Gly Val Trp Arg Phe Leu Ala Ser Arg Asp Ser Glu Pro Gln Ala Ser
65 70 75 80

Ser Ala Thr Ser Pro Phe Asp Arg Leu Gln Val Gln Gly Asp Gly Ser
85 90 95

Ala Pro Leu Ser Phe Phe Pro Thr Ala Ser Ala Pro Asn Val Gln Pro
100 105 110

Pro Pro Ser Ser Gly Gly Arg Asp Arg Asp Gln Gln Asn His Val Ile
115 120 125

Arg Val Val Pro Arg Asn Ala Gln Thr Ala Ser Val Pro Lys Ala Gln
130 135 140

Pro Gln Pro Ser Ser Gly Gly Arg Asp Gln Lys Asn His Val Ile Arg
145 150 155 160

Val Val Pro His Asn Ala Gln Thr Ala Ser Glu Ser Ala Ala Trp Ile
165 170 175

Phe Arg Ser Ile Gln Met Glu Arg Asn Gln Asn Asp Ser
180 185

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aaccaaccaa taccttccac gtcatgtaca atccgagttc ccgtgagata gggatcttta 120

cttgaagcaa ccagacatga ccgcagagtc acacacacac acacccctaa gctttttgtc 180

gtcccctcgt atggaatcca ttgtgggacg acacaaaaat atcttctttt gcttctctgc 240

tttcttcttc ttcttcttaa aatttgtttc tttcaggtgg atttgatctc catctacgta 300

aaacaaaaac aaagtttata atctttttgg attttgggat tgatctaaag tgagatttcg 360

atcttggcac taggttttgc aaggttacct aacaatttct ggttctgatt tcatttcttt 420

aggttacgtg taagggaagg aattgttaat agggtttgtt tgtgagcgta gggaaaag 478

atg gga gga atg aaa gat gaa gca aag agg ata aca att cct cca ttg 526
Met Gly Gly Met Lys Asp Glu Ala Lys Arg Ile Thr Ile Pro Pro Leu
1 5 10 15

ttt cca agg gtt cat gtc aat gat act gga aga gga ggc ctg tct caa 574
Phe Pro Arg Val His Val Asn Asp Thr Gly Arg Gly Gly Leu Ser Gln
20 25 30

caa ttt gat ggc aaa aca atg tct ctc gtc tct tct aaa cgt ccc aat 622
Gln Phe Asp Gly Lys Thr Met Ser Leu Val Ser Ser Lys Arg Pro Asn
35 40 45

ctt cct tct ccg acc aac aac ata tct gat tct ctt tcc act ttc tct 670
Leu Pro Ser Pro Thr Asn Asn Ile Ser Asp Ser Leu Ser Thr Phe Ser
50 55 60

ttg tct ctt cct cca cca cca aac aat gcc cgt ctc gtgagtcctt 716
Leu Ser Leu Pro Pro Pro Pro Asn Asn Ala Arg Leu
65 70 75

ttaattcact cattcaactt tcttggtttt gtgtgtctgc agatttatat acaagaatgg 776

tgacaatgca tatttagatt atcactttat gacttgttga atacttttt gtaacag 833

att gat gga cct gaa aag aat cag ttt tca cca atc tac aac aca aag 881
Ile Asp Gly Pro Glu Lys Asn Gln Phe Ser Pro Ile Tyr Asn Thr Lys
80 85 90

ttt gag ggg aag ctg aat aaa aaa ggc ata aat tat aca agt cct aaa 929
Phe Glu Gly Lys Leu Asn Lys Lys Gly Ile Asn Tyr Thr Ser Pro Lys
95 100 105

gga tca tca gtt act aat act aag cct agt tca ata aaa caa aat gag 977
Gly Ser Ser Val Thr Asn Thr Lys Pro Ser Ser Ile Lys Gln Asn Glu
110 115 120

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tac ctc aag aac ctt acc agc ttg gat tct att aag tct cct att gtt     1025
Tyr Leu Lys Asn Leu Thr Ser Leu Asp Ser Ile Lys Ser Pro Ile Val
125                 130                 135                 140

ata cac tca gaa ata gat cca caa gca aac aca gat ttg tca ctc caa     1073
Ile His Ser Glu Ile Asp Pro Gln Ala Asn Thr Asp Leu Ser Leu Gln
                145                 150                 155

ttt tgt act agc ggt agc agt aaa ccc gga gga gag gct gtt gtt ggt     1121
Phe Cys Thr Ser Gly Ser Ser Lys Pro Gly Gly Glu Ala Val Val Gly
            160                 165                 170

tct aag atc ctt ttg tca gaa cgt ttg gaa gat gaa aac cag aat ggg     1169
Ser Lys Ile Leu Leu Ser Glu Arg Leu Glu Asp Glu Asn Gln Asn Gly
        175                 180                 185

tct ccc aat gtg atg aaa act caa tca tat aga aga aac ttt gct gag     1217
Ser Pro Asn Val Met Lys Thr Gln Ser Tyr Arg Arg Asn Phe Ala Glu
    190                 195                 200

ttt aac aat gaa act caa aag aag ccc aaa act ctg cct cgg cgt gaa     1265
Phe Asn Asn Glu Thr Gln Lys Lys Pro Lys Thr Leu Pro Arg Arg Glu
205                 210                 215                 220

caa gtt gct tca aac tgc tct gca ata gag tct ttg tct ggt ata agt     1313
Gln Val Ala Ser Asn Cys Ser Ala Ile Glu Ser Leu Ser Gly Ile Ser
                225                 230                 235

gca tct tct tat gat att gcc aga gtg att ggt gaa aag agg ttt tgg     1361
Ala Ser Ser Tyr Asp Ile Ala Arg Val Ile Gly Glu Lys Arg Phe Trp
            240                 245                 250

aag atg aga aca tat atg atc aa  gtttgtatcc tcctctcact tttcttatga    1414
Lys Met Arg Thr Tyr Met Ile Asn
        255

tcccaacttc ataactttgc cgtatttctt actatttttt attgttgata ttttcag t    1472

cag caa aag atc ttt gcc ggg caa gta ttt gag ctc cat aga ctg ata     1520
Gln Gln Lys Ile Phe Ala Gly Gln Val Phe Glu Leu His Arg Leu Ile
                265                 270                 275

atg gtaagctttt aataacctta ttgtttctgg tttgctttct atgcttcaga          1573
Met


ttacttaata tgatgcag gtt caa aag atg gtt gcg aag tcg cca aac ttg     1624
                    Val Gln Lys Met Val Ala Lys Ser Pro Asn Leu
                            280                 285

ttt ctt gaa agt aag ctt aat ggt gtc aaa cat ggt aca atg agg tca     1672
Phe Leu Glu Ser Lys Leu Asn Gly Val Lys His Gly Thr Met Arg Ser
    290                 295                 300

tca cat cag ctt gca atg gcg gct tca aag gtt aga aag cca aac act     1720
Ser His Gln Leu Ala Met Ala Ala Ser Lys Val Arg Lys Pro Asn Thr
305                 310                 315                 320
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gag aat cac aaa cct gta cct gaa gaa tat cca gag cat atg aaa cca     1768
Glu Asn His Lys Pro Val Pro Glu Glu Tyr Pro Glu His Met Lys Pro
                325                 330                 335

aag ctt cct cta cct tcc ata agc aaa gaa ctc gtg act cct att tgg     1816
Lys Leu Pro Leu Pro Ser Ile Ser Lys Glu Leu Val Thr Pro Ile Trp
            340                 345                 350

cca caa cag cta ctt cct cct cct gga aac caa tgg tta gtt cct gta     1864
Pro Gln Gln Leu Leu Pro Pro Pro Gly Asn Gln Trp Leu Val Pro Val
        355                 360                 365

ata act gat tca gac ggt ctg gtc tat aaa cca ttt cca gga cca tgt     1912
Ile Thr Asp Ser Asp Gly Leu Val Tyr Lys Pro Phe Pro Gly Pro Cys
    370                 375                 380

cct cct tct tct tca gcc ttc atg gtt cca gtt tat ggc caa gat tca     1960
Pro Pro Ser Ser Ser Ala Phe Met Val Pro Val Tyr Gly Gln Asp Ser
385                 390                 395                 400

ctc gag aca cca ttc agg ttc cct gtt tct tct cca ttc agc cac agc     2008
Leu Glu Thr Pro Phe Arg Phe Pro Val Ser Ser Pro Phe Ser His Ser
                405                 410                 415

tac ttc cca cct cct aac gcg agg aca aca gtt gac caa aca aac ccg     2056
Tyr Phe Pro Pro Pro Asn Ala Arg Thr Thr Val Asp Gln Thr Asn Pro
            420                 425                 430

ttt ggt cag ttt caa aga tgg tct aac aca tca agc cac atg aca caa     2104
Phe Gly Gln Phe Gln Arg Trp Ser Asn Thr Ser Ser His Met Thr Gln
        435                 440                 445

gcc att cca ttt tct tta aag aag tct cag gaa tct aat gac agt gac     2152
Ala Ile Pro Phe Ser Leu Lys Lys Ser Gln Glu Ser Asn Asp Ser Asp
    450                 455                 460

ata cat gga agc aca gct tca agt cca cca gag aag cat aaa ctt gaa     2200
Ile His Gly Ser Thr Ala Ser Ser Pro Pro Glu Lys His Lys Leu Glu
465                 470                 475                 480

gtg ctt cct ctg ttt cct aca gag cct acc cat caa act gat gag tac     2248
Val Leu Pro Leu Phe Pro Thr Glu Pro Thr His Gln Thr Asp Glu Tyr
                485                 490                 495

aag cag aaa cag caa ccg atg ctt cgc gcc att aaa gcc gtt cct cat     2296
Lys Gln Lys Gln Gln Pro Met Leu Arg Ala Ile Lys Ala Val Pro His
            500                 505                 510

aat tca aca tct gcc tct gaa tct gct gca agg atc ttc cgt ttc att     2344
Asn Ser Thr Ser Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Phe Ile
        515                 520                 525

cag gaa gaa agg agg gac tca gat cat atg att agt tag ttcttttata     2393
Gln Glu Glu Arg Arg Asp Ser Asp His Met Ile Ser
    530                 535                 540
```

tttgaaaccc ttccacattc ttttgctctc attgcttctt catctagctt agattttcag 2453

tatattctat ttactcttct tatgaagatg taaatcaaat actatcacta tacattaaac 2513

atacacacac ttatacacac atcttacatt gttcttgtat tgacaaacag ctaataaaag 2573

atagactttt gtgcttctat tccagttttg aggagtttaa acattggaac aagaagagtt 2633

ctttagccat tgaagtatct atattatcaa tgtggaagga gacaataagg atcagagttg 2693

tgtccatgct atacgaagct acactcaagt tcaagaacat ttcagaacaa aaaccaagaa 2753

caaaaagaag acaagagatc cattaattag aacccaagaa c 2794

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Phe Pro Arg Val His Val Asn Asp Thr Gly Arg Gly Gly Leu Ser Gln
20 25 30

Gln Phe Asp Gly Lys Thr Met Ser Leu Val Ser Ser Lys Arg Pro Asn
35 40 45

Leu Pro Ser Pro Thr Asn Asn Ile Ser Asp Ser Leu Ser Thr Phe Ser
50 55 60

Leu Ser Leu Pro Pro Pro Pro Asn Asn Ala Arg Leu Ile Asp Gly Pro
65 70 75 80

Glu Lys Asn Gln Phe Ser Pro Ile Tyr Asn Thr Lys Phe Glu Gly Lys
85 90 95

Leu Asn Lys Lys Gly Ile Asn Tyr Thr Ser Pro Lys Gly Ser Ser Val
100 105 110

Thr Asn Thr Lys Pro Ser Ser Ile Lys Gln Asn Glu Tyr Leu Lys Asn
115 120 125

Leu Thr Ser Leu Asp Ser Ile Lys Ser Pro Ile Val Ile His Ser Glu
130 135 140

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Ile Asp Pro Gln Ala Asn Thr Asp Leu Ser Leu Gln Phe Cys Thr Ser
145                 150                 155                 160

Gly Ser Ser Lys Pro Gly Gly Glu Ala Val Val Gly Ser Lys Ile Leu
                165                 170                 175

Leu Ser Glu Arg Leu Glu Asp Glu Asn Gln Asn Gly Ser Pro Asn Val
            180                 185                 190

Met Lys Thr Gln Ser Tyr Arg Arg Asn Phe Ala Glu Phe Asn Asn Glu
        195                 200                 205

Thr Gln Lys Lys Pro Lys Thr Leu Pro Arg Arg Glu Gln Val Ala Ser
    210                 215                 220

Asn Cys Ser Ala Ile Glu Ser Leu Ser Gly Ile Ser Ala Ser Ser Tyr
225                 230                 235                 240

Asp Ile Ala Arg Val Ile Gly Glu Lys Arg Phe Trp Lys Met Arg Thr
                245                 250                 255

Tyr Met Ile Asn Gln Gln Lys Ile Phe Ala Gly Gln Val Phe Glu Leu
            260                 265                 270

His Arg Leu Ile Met Val Gln Lys Met Val Ala Lys Ser Pro Asn Leu
        275                 280                 285

Phe Leu Glu Ser Lys Leu Asn Gly Val Lys His Gly Thr Met Arg Ser
    290                 295                 300

Ser His Gln Leu Ala Met Ala Ala Ser Lys Val Arg Lys Pro Asn Thr
305                 310                 315                 320

Glu Asn His Lys Pro Val Pro Glu Glu Tyr Pro Glu His Met Lys Pro
                325                 330                 335

Lys Leu Pro Leu Pro Ser Ile Ser Lys Glu Leu Val Thr Pro Ile Trp
            340                 345                 350

Pro Gln Gln Leu Leu Pro Pro Pro Gly Asn Gln Trp Leu Val Pro Val
        355                 360                 365
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Ile Thr Asp Ser Asp Gly Leu Val Tyr Lys Pro Phe Pro Gly Pro Cys
    370                 375                 380

Pro Pro Ser Ser Ser Ala Phe Met Val Pro Val Tyr Gly Gln Asp Ser
385                 390                 395                 400

Leu Glu Thr Pro Phe Arg Phe Pro Val Ser Ser Pro Phe Ser His Ser
                405                 410                 415

Tyr Phe Pro Pro Pro Asn Ala Arg Thr Thr Val Asp Gln Thr Asn Pro
            420                 425                 430

Phe Gly Gln Phe Gln Arg Trp Ser Asn Thr Ser Ser His Met Thr Gln
        435                 440                 445

Ala Ile Pro Phe Ser Leu Lys Lys Ser Gln Glu Ser Asn Asp Ser Asp
    450                 455                 460

Ile His Gly Ser Thr Ala Ser Ser Pro Pro Glu Lys His Lys Leu Glu
465                 470                 475                 480

Val Leu Pro Leu Phe Pro Thr Glu Pro Thr His Gln Thr Asp Glu Tyr
                485                 490                 495

Lys Gln Lys Gln Gln Pro Met Leu Arg Ala Ile Lys Ala Val Pro His
            500                 505                 510

Asn Ser Thr Ser Ala Ser Glu Ser Ala Ala Arg Ile Phe Arg Phe Ile
        515                 520                 525

Gln Glu Glu Arg Arg Asp Ser Asp His Met Ile Ser
    530                 535                 540
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ctctgtttct cgattagtac gttgaaaact cacttkggtt ttgtttgatt cctctttagt 180

ctgtttttcg atttcgtttt ctctgattgg tttggtggtg agatctctat cgtagtttgt 240

cctttgggtt aagatatttc atttgattgg tgggtttgtt ttattgaagc ttattgttgt 300

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gaaagttgga gtctttctca gtttttaggt tgaattatta agagaaaggg aagatttttg    360

gtgtgaagtt aggttatttg gggtttgaga agtttgcaag tgaaaaaggt tgtgaattgt    420

gagtg atg aag aga ggg aaa gat gag gag aag ata ttg gaa cct atg ttt    470
      Met Lys Arg Gly Lys Asp Glu Glu Lys Ile Leu Glu Pro Met Phe
      1               5                  10                  15

cct cgg ctt cat gtg aat gat gca gat aaa gga ggg cct aga gct cct      518
Pro Arg Leu His Val Asn Asp Ala Asp Lys Gly Gly Pro Arg Ala Pro
                20                  25                  30

cct aga aac aag atg gct ctt tat gag cag ctt agt att cct tct cag      566
Pro Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln
            35                  40                  45

agg ttt ggt gat cat gga acg atg aat tct cgt agt aac aac aca agc      614
Arg Phe Gly Asp His Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser
        50                  55                  60

act ttg gtt cat cct gga cca tct agt cag gtattgtttt gattttgatc        664
Thr Leu Val His Pro Gly Pro Ser Ser Gln
    65                  70

attgtatagg ctcttgatgt tattagttgt atgagtttgg atgttatata gcctgaaaga    724

gaaagtagga cattggttga tctatgtttc aattgttatc agatcatagt atcttctttt    784

tgcttatgga ttgagctttt aggattgaat tctcctgtat atatgagagt cttgtagaca    844

caagtttatc taagtgtggt ttatttctta aaactaacat tcttgttgtg cctgattctt    904

tttatgttct gaagttcgat gaaagtttct tgtgattgcc ctgagcattc agactattgc    964

aaggacatga gaaataatcc ttttttaccc tcttcaatgc ag cct tgt ggt gtg      1018
                                              Pro Cys Gly Val
                                                  75

gaa aga aac tta tct gtc cag cat ctt gat tct tca gcc gca aac caa     1066
Glu Arg Asn Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Asn Gln
        80                  85                  90

gca act gag aag ttt gtc tcc caa atg tcc ttc atg gaa aat gtg aga     1114
Ala Thr Glu Lys Phe Val Ser Gln Met Ser Phe Met Glu Asn Val Arg
    95                  100                 105

tct tcg gca cag cat gat cag agg aaa atg gtg aga gag gaa gaa gat     1162
Ser Ser Ala Gln His Asp Gln Arg Lys Met Val Arg Glu Glu Glu Asp
110                 115                 120                 125

ttt gca gtt cca gta tat att aac tca aga aga tct cag tct cat ggc     1210
Phe Ala Val Pro Val Tyr Ile Asn Ser Arg Arg Ser Gln Ser His Gly
                130                 135                 140

aga acc aag agt ggt att gag aag gaa aaa cac acc cca atg gtg gca     1258
Arg Thr Lys Ser Gly Ile Glu Lys Glu Lys His Thr Pro Met Val Ala
            145                 150                 155
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Pro Ser Ser His His Ser Ile Arg Phe Gln Glu Val Asn Gln Thr Gly
        160                 165                 170

tca aag caa aac gta tgt ttg gct act tgt tca aaa cct gaa gtt agg     1354
Ser Lys Gln Asn Val Cys Leu Ala Thr Cys Ser Lys Pro Glu Val Arg
    175                 180                 185

gat cag gtc aag gcg aat gca agg tca ggt ggc ttt gta atc tct tta     1402
Asp Gln Val Lys Ala Asn Ala Arg Ser Gly Gly Phe Val Ile Ser Leu
190                 195                 200                 205

gat gta tca gtc aca gag gag att gat ctc gaa aaa tca gca tca agt     1450
Asp Val Ser Val Thr Glu Glu Ile Asp Leu Glu Lys Ser Ala Ser Ser
                210                 215                 220

cat gat aga gta aat gat tat aat gct tcc ttg aga caa gag tct aga     1498
His Asp Arg Val Asn Asp Tyr Asn Ala Ser Leu Arg Gln Glu Ser Arg
            225                 230                 235

aat cgg tta tac cga gat ggt ggc aaa act cgt ctg aag gac act gat     1546
Asn Arg Leu Tyr Arg Asp Gly Gly Lys Thr Arg Leu Lys Asp Thr Asp
        240                 245                 250

aat gga gct gaa tct cac ttg gca acg gaa aat cat tca caa gag ggt     1594
Asn Gly Ala Glu Ser His Leu Ala Thr Glu Asn His Ser Gln Glu Gly
    255                 260                 265

cat ggc agt cct gaa gac att gat aat gat cgt gaa tac agc aaa agc     1642
His Gly Ser Pro Glu Asp Ile Asp Asn Asp Arg Glu Tyr Ser Lys Ser
270                 275                 280                 285

aga gca tgc gcc tct ctg cag cag ata aat gaa gag gca agt gat gac     1690
Arg Ala Cys Ala Ser Leu Gln Gln Ile Asn Glu Glu Ala Ser Asp Asp
                290                 295                 300

gtt tct gat gat tcg atg gtg gat tct ata tcc agc ata gat gtc tct     1738
Val Ser Asp Asp Ser Met Val Asp Ser Ile Ser Ser Ile Asp Val Ser
            305                 310                 315

ccc gat gat gtt gtg ggt ata tta ggt caa aaa cgt ttc tgg aga gca     1786
Pro Asp Asp Val Val Gly Ile Leu Gly Gln Lys Arg Phe Trp Arg Ala
        320                 325                 330

agg aaa gcc att gcc aa  gtaagttcac tagaaattta cagtttggtt            1833
Arg Lys Ala Ile Ala Asn
    335

atttattctc cgctctttct atttatctcc ttctttgata ccaacatttt ttgcttgaaa   1893

gaagttaata tttaagcatt gttccgtagt cttactgaag ctttttcctc tgttgttttt   1953

tgctattttc attgaggact gtggtagggc atatttcact atcaccaaat ttcaaatttc   2013

tagaacactc tccttcatat ttttttttcat gattaatgct gcaattgatt gctgatatac   2073
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atatatgact ataactcagt ttcatattct gtctcatttt gggagaaaga gatttcaggt   2133

ttatgcttga gaagtgatgg ttctatagtt gagaggcccc tgattcatct aaaatggtcc   2193

tattatgtgt ttagttgtag agtcctcggt agaatattaa cgcgtttaac acgttggatc   2253

atgttatagc agggagggac attctctgtt gacctatatt gtgcaaggtg cccgccgatg   2313

gctttattac tataccttct ttgcatctgg ttgttggaac atgtccctgt ctcggtttgg   2373

tattgctttt attctgcact gtcgtcttgg gcattttccc tacttgtcat tcaaggggtt   2433

gaaccaggta gggaaatgtt tttccgagga ccccaggatc taaattttag ttaaccatac   2493

gtaaagttag ttttgagtct tatgacgatg cagaattata gtttcttctt actactgctt   2553

aagaggatcc ttagtgtggt tgtgaactac agagttttta tgattgtagg cttcatgact   2613

taacttttaa ggttcaatgt actctaatcc atatggtaag gtatcggatt cacgaccaat   2673

gcaaataata agatttttat ttcttgcttc ttgttaaata tctgacatct cattttgcag   2733

aggataagct gcgctgtaag ctagatttca ataagcccgt cctttgcatt gttatctatg   2793

ctttaatatg tcattggacc cattgatttg gttttcttct atctttttg attggctatg   2853

tattcttgtt tctttttcc tatctcattt cgatcgtatt gttccattag ctgttcaacc   2913

taaactatgt ctctctttgt tgaacttttg atggataatc ttcttaatgt gactctgttt   2973

ctcattacag t caa caa aga gta ttt gct gtt caa cta ttt gag ttg cac   3023
            Gln Gln Arg Val Phe Ala Val Gln Leu Phe Glu Leu His
            340                 345                 350

aga ctg att aag gtaaagtcat tcagaaactt ctcatatgtt tccatgagta       3075
Arg Leu Ile Lys
        355

tttgtttctt ctcgagctga aacaaacctc ttcaactgtg taataatcag gtt caa     3131
                                                        Val Gln


aaa ctt att gct gca tca ccg gat ctc ttg ctc gat gag atc agt ttt   3179
Lys Leu Ile Ala Ala Ser Pro Asp Leu Leu Leu Asp Glu Ile Ser Phe
    360                 365                 370

ctt gga aaa gtt tct gct aaa agc tat cca gtg aag aag ctc ctt cca   3227
Leu Gly Lys Val Ser Ala Lys Ser Tyr Pro Val Lys Lys Leu Leu Pro
375                 380                 385                 390

tca gaa ttt ctg gta aag cct cct cta cca cat gtt gtc gtc aaa caa   3275
Ser Glu Phe Leu Val Lys Pro Pro Leu Pro His Val Val Val Lys Gln
                395                 400                 405

agg ggt gac tcg gag aag act gac caa cat aaa atg gaa agc tca gct   3323
Arg Gly Asp Ser Glu Lys Thr Asp Gln His Lys Met Glu Ser Ser Ala
            410                 415                 420
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gag aac gta gtt ggg agg ttg tca aat caa ggt cat cat caa caa tcc     3371
Glu Asn Val Val Gly Arg Leu Ser Asn Gln Gly His His Gln Gln Ser
        425                 430                 435

aac tac atg cct ttt gca aac aac cca ccg gct tca ccg gct cca aat     3419
Asn Tyr Met Pro Phe Ala Asn Asn Pro Pro Ala Ser Pro Ala Pro Asn
    440                 445                 450

gga tat tgc ttt cct cct cag cct cct cct tca gga aat cat cag caa     3467
Gly Tyr Cys Phe Pro Pro Gln Pro Pro Pro Ser Gly Asn His Gln Gln
455                 460                 465                 470

tgg ttg atc cct gta atg tct ccc tcg gaa gga ctg ata tac aag cct     3515
Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Ile Tyr Lys Pro
                475                 480                 485

cac cca ggt atg gca cac acg ggg cat tat gga gga tat tat ggt cat     3563
His Pro Gly Met Ala His Thr Gly His Tyr Gly Gly Tyr Tyr Gly His
            490                 495                 500

tat atg cct aca cca atg gta atg cct caa tat cac ccc ggc atg gga     3611
Tyr Met Pro Thr Pro Met Val Met Pro Gln Tyr His Pro Gly Met Gly
        505                 510                 515

ttc cca cct cct ggt aat ggc tac ttc cct cca tat gga atg atg ccc     3659
Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro Pro Tyr Gly Met Met Pro
    520                 525                 530

acc ata atg aac cca tat tgt tca agc caa caa caa caa caa caa caa     3707
Thr Ile Met Asn Pro Tyr Cys Ser Ser Gln Gln Gln Gln Gln Gln Gln
535                 540                 545                 550

ccc aat gag caa atg aac cag ttt gga cat cct gga aat ctt cag aac     3755
Pro Asn Glu Gln Met Asn Gln Phe Gly His Pro Gly Asn Leu Gln Asn
                555                 560                 565

acc caa caa caa caa cag aga tct gat aat gaa cct gct cca cag caa     3803
Thr Gln Gln Gln Gln Gln Arg Ser Asp Asn Glu Pro Ala Pro Gln Gln
            570                 575                 580

cag caa cag cca aca aag tct tat ccg cga gca aga aag agc agg caa     3851
Gln Gln Gln Pro Thr Lys Ser Tyr Pro Arg Ala Arg Lys Ser Arg Gln
        585                 590                 595

ggg agc aca gga agc agt cca agt ggg cca cag gga atc tct ggt agc     3899
Gly Ser Thr Gly Ser Ser Pro Ser Gly Pro Gln Gly Ile Ser Gly Ser
    600                 605                 610

aag tcc ttt cgg cca ttc gca gcc gtt gat gag gac agc aac atc aac     3947
Lys Ser Phe Arg Pro Phe Ala Ala Val Asp Glu Asp Ser Asn Ile Asn
615                 620                 625                 630

aat gca cct gag caa acg atg aca aca acc aca acg acg aca aga aca     3995
Asn Ala Pro Glu Gln Thr Met Thr Thr Thr Thr Thr Thr Thr Arg Thr
                635                 640                 645
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act gtt act cag aca aca aga gat ggg gga gga gtg acg aga gtg ata 4043
Thr Val Thr Gln Thr Thr Arg Asp Gly Gly Gly Val Thr Arg Val Ile
650 655 660

aag gtg gta cct cac aac gca aag ctc gcg agt gag aat gct gcc aga 4091
Lys Val Val Pro His Asn Ala Lys Leu Ala Ser Glu Asn Ala Ala Arg
665 670 675

att ttc cag tca ata caa gaa gaa cgt aaa cgc tat gac tcc tct aag 4139
Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys Arg Tyr Asp Ser Ser Lys
680 685 690

cct taa tcctctctat gcgtattgta cttgatatgt attttacaaa attagaaaaa 4195
Pro
695

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20 25 30

Arg Asn Lys Met Ala Leu Tyr Glu Gln Leu Ser Ile Pro Ser Gln Arg
35 40 45

Phe Gly Asp His Gly Thr Met Asn Ser Arg Ser Asn Asn Thr Ser Thr
50 55 60

Leu Val His Pro Gly Pro Ser Ser Gln Pro Cys Gly Val Glu Arg Asn
65 70 75 80

Leu Ser Val Gln His Leu Asp Ser Ser Ala Ala Asn Gln Ala Thr Glu
85 90 95

Lys Phe Val Ser Gln Met Ser Phe Met Glu Asn Val Arg Ser Ser Ala
100 105 110

Gln His Asp Gln Arg Lys Met Val Arg Glu Glu Glu Asp Phe Ala Val
115 120 125

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Pro Val Tyr Ile Asn Ser Arg Arg Ser Gln Ser His Gly Arg Thr Lys
    130                 135                 140

Ser Gly Ile Glu Lys Glu Lys His Thr Pro Met Val Ala Pro Ser Ser
145                 150                 155                 160

His His Ser Ile Arg Phe Gln Glu Val Asn Gln Thr Gly Ser Lys Gln
                165                 170                 175

Asn Val Cys Leu Ala Thr Cys Ser Lys Pro Glu Val Arg Asp Gln Val
            180                 185                 190

Lys Ala Asn Ala Arg Ser Gly Gly Phe Val Ile Ser Leu Asp Val Ser
        195                 200                 205

Val Thr Glu Glu Ile Asp Leu Glu Lys Ser Ala Ser Ser His Asp Arg
    210                 215                 220

Val Asn Asp Tyr Asn Ala Ser Leu Arg Gln Glu Ser Arg Asn Arg Leu
225                 230                 235                 240

Tyr Arg Asp Gly Gly Lys Thr Arg Leu Lys Asp Thr Asp Asn Gly Ala
                245                 250                 255

Glu Ser His Leu Ala Thr Glu Asn His Ser Gln Glu Gly His Gly Ser
            260                 265                 270

Pro Glu Asp Ile Asp Asn Asp Arg Glu Tyr Ser Lys Ser Arg Ala Cys
        275                 280                 285

Ala Ser Leu Gln Gln Ile Asn Glu Glu Ala Ser Asp Asp Val Ser Asp
    290                 295                 300

Asp Ser Met Val Asp Ser Ile Ser Ser Ile Asp Val Ser Pro Asp Asp
305                 310                 315                 320

Val Val Gly Ile Leu Gly Gln Lys Arg Phe Trp Arg Ala Arg Lys Ala
                325                 330                 335

Ile Ala Asn Gln Gln Arg Val Phe Ala Val Gln Leu Phe Glu Leu His
            340                 345                 350
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Arg Leu Ile Lys Val Gln Lys Leu Ile Ala Ala Ser Pro Asp Leu Leu
355 360 365

Leu Asp Glu Ile Ser Phe Leu Gly Lys Val Ser Ala Lys Ser Tyr Pro
370 375 380

Val Lys Lys Leu Leu Pro Ser Glu Phe Leu Val Lys Pro Pro Leu Pro
385 390 395 400

His Val Val Val Lys Gln Arg Gly Asp Ser Glu Lys Thr Asp Gln His
405 410 415

Lys Met Glu Ser Ser Ala Glu Asn Val Val Gly Arg Leu Ser Asn Gln
420 425 430

Gly His His Gln Gln Ser Asn Tyr Met Pro Phe Ala Asn Asn Pro Pro
435 440 445

Ala Ser Pro Ala Pro Asn Gly Tyr Cys Phe Pro Pro Gln Pro Pro Pro
450 455 460

Ser Gly Asn His Gln Gln Trp Leu Ile Pro Val Met Ser Pro Ser Glu
465 470 475 480

Gly Leu Ile Tyr Lys Pro His Pro Gly Met Ala His Thr Gly His Tyr
485 490 495

Gly Gly Tyr Tyr Gly His Tyr Met Pro Thr Pro Met Val Met Pro Gln
500 505 510

Tyr His Pro Gly Met Gly Phe Pro Pro Pro Gly Asn Gly Tyr Phe Pro
515 520 525

Pro Tyr Gly Met Met Pro Thr Ile Met Asn Pro Tyr Cys Ser Ser Gln
530 535 540

Gln Gln Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Gln Phe Gly His
545 550 555 560

Pro Gly Asn Leu Gln Asn Thr Gln Gln Gln Gln Gln Arg Ser Asp Asn
565 570 575

Glu Pro Ala Pro Gln Gln Gln Gln Gln Pro Thr Lys Ser Tyr Pro Arg

580 585 590

Ala Arg Lys Ser Arg Gln Gly Ser Thr Gly Ser Ser Pro Ser Gly Pro
595 600 605

Gln Gly Ile Ser Gly Ser Lys Ser Phe Arg Pro Phe Ala Ala Val Asp
610 615 620

Glu Asp Ser Asn Ile Asn Asn Ala Pro Glu Gln Thr Met Thr Thr Thr
625 630 635 640

Thr Thr Thr Thr Arg Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Gly
645 650 655

Gly Val Thr Arg Val Ile Lys Val Val Pro His Asn Ala Lys Leu Ala
660 665 670

Ser Glu Asn Ala Ala Arg Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys
675 680 685

Arg Tyr Asp Ser Ser Lys Pro
690 695

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aatttcctcc atcgattttg ataaattttt ttaatactac aaactataag caagatcaag 180

tatgaatttt atgtttttct gatacccagt tgggaaaagt ttagattttg tgaattagtt 240

gtgttaatta gtgattagta tagttctgtg tatatgctat aatcactttt tatttttttgg 300

agttcaggat tataaactga ttctgttctt tgagtgtaat tattgatttg gttgatccat 360

agctgtatta ggaaggttaa gg atg aag aga ggg aat gat gat gag aaa gtg 412
Met Lys Arg Gly Asn Asp Asp Glu Lys Val
1 5 10

ang ggg ccg tta ttn cct agg tta cat gtt ggt gat aca gag aag gga 460
Xaa Gly Pro Leu Xaa Pro Arg Leu His Val Gly Asp Thr Glu Lys Gly
15 20 25

ggg cca aga gca cct cct agg aat aaa ttg gct ctc tat gag caa ttt 508
Gly Pro Arg Ala Pro Pro Arg Asn Lys Leu Ala Leu Tyr Glu Gln Phe
30 35 40

aa 510

<210> 37
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Met Lys Arg Gly Asn Asp Asp Glu Lys Val Xaa Gly Pro Leu Phe Pro
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Arg Leu His Val Gly Asp Thr Glu Lys Gly Gly Pro Arg Ala Pro Pro
20 25 30

Arg Asn Lys Leu Ala Leu Tyr Glu Gln Phe
35 40

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Arg Val Ile Lys Val Val Pro His Asn Arg Arg Ser Ala Thr Glu Ser
1 5 10 15

gca gct aga att ttc caa tca att caa gaa gag aga aaa caa tat gac 97
Ala Ala Arg Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys Gln Tyr Asp
20 25 30

aca ctc tag tgctgtttat tctcatggag gatccattca agtgtaaggt 146
Thr Leu

gtctagttcc tgtactttct gcacgtgtgg catcgtgtaa aggtatatta tattatatat 206

atttttttgtt ttgaccttct tattttcagc acagtggtat gtagatatgt ctggcatatc 266

aaaattggtc aaaacatgat ctattgtacg ttatcctctt aagtacttgt acgtttctca 326

caggaatcga atcacaggaa aaagttagta gttctcagct ccgctccctt tgcttgggag 386

gaggtttttg atcctatgta ctacttggct ttaaaattgg tgattgtcag tgttgggttt 446

tattctagtt ctatttttgt tatttaatgt atgacaaatt ctatcttaaa caatttcgta 506

gcttgtgagg gggtgttaaa gtcttacaag gaagaggcat tgttagttat tggtcgagtc 566

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<213> Medicago truncatula

<400> 39

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1 5 10 15

Ala Ala Arg Ile Phe Gln Ser Ile Gln Glu Glu Arg Lys Gln Tyr Asp
20 25 30

Thr Leu

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Gln Thr Asp Lys
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Val Gln His Leu Ile
5

gct gaa tca tca aat ctt ttg ccc gat act gct gct gtt ttg gga aaa 155
Ala Glu Ser Ser Asn Leu Leu Pro Asp Thr Ala Ala Val Leu Gly Lys
10 15 20 25

cct ctt ctg cag gga tct aat tct aaa agc ctt tca ttt gaa gaa gtt 203
Pro Leu Leu Gln Gly Ser Asn Ser Lys Ser Leu Ser Phe Glu Glu Val
30 35 40

gtt gaa cct cag gca caa aat cat aaa cag caa gac cat tct gaa aac 251

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Val Glu Pro Gln Ala Gln Asn His Lys Gln Gln Asp His Ser Glu Asn
            45                  50                  55

caa aac cat aaa ttg gat tat tct act gaa aat gga gtt ggg aaa aca      299
Gln Asn His Lys Leu Asp Tyr Ser Thr Glu Asn Gly Val Gly Lys Thr
        60                  65                  70

tcc tta tca tcc caa aaa tca aac cag gca aat gct ggt tca cag tgt      347
Ser Leu Ser Ser Gln Lys Ser Asn Gln Ala Asn Ala Gly Ser Gln Cys
    75                  80                  85

ttt aat caa tca cct gga cat                                         368
Phe Asn Gln Ser Pro Gly His
90                  95
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<210> 41
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<213> Pisum sativum

<400> 41

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Pro Asp Thr Ala Ala Val Leu Gly Lys Pro Leu Leu Gln Gly Ser Asn
            20                  25                  30

Ser Lys Ser Leu Ser Phe Glu Glu Val Val Glu Pro Gln Ala Gln Asn
        35                  40                  45

His Lys Gln Gln Asp His Ser Glu Asn Gln Asn His Lys Leu Asp Tyr
    50                  55                  60

Ser Thr Glu Asn Gly Val Gly Lys Thr Ser Leu Ser Ser Gln Lys Ser
65                  70                  75                  80

Asn Gln Ala Asn Ala Gly Ser Gln Cys Phe Asn Gln Ser Pro Gly His
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tac gcg gct gct cct tcg ggt ggc act ttt atg aat cct tcc tat gga 97
Tyr Ala Ala Ala Pro Ser Gly Gly Thr Phe Met Asn Pro Ser Tyr Gly
20 25 30

atc ccg cct cca cca gag act cct cca ggc agt caa gct tac ttc cct 145
Ile Pro Pro Pro Pro Glu Thr Pro Pro Gly Ser Gln Ala Tyr Phe Pro
35 40 45

ccc tac ggt ggc atg cca gtt atg aaa gct gca gct tca gag tca gct 193
Pro Tyr Gly Gly Met Pro Val Met Lys Ala Ala Ala Ser Glu Ser Ala
50 55 60

gtt gaa cat gtg aac caa ttc tcc gca cgc ggg caa agt cgt cgt tta 241
Val Glu His Val Asn Gln Phe Ser Ala Arg Gly Gln Ser Arg Arg Leu
65 70 75 80

tct gaa gat gaa gct gat tgt aac aaa cac aat caa agc tca tac gat 289
Ser Glu Asp Glu Ala Asp Cys Asn Lys His Asn Gln Ser Ser Tyr Asp
85 90 95

tta cca gtt cag aga aat gga gct aca tca cat gtc atg tat cat cag 337
Leu Pro Val Gln Arg Asn Gly Ala Thr Ser His Val Met Tyr His Gln
100 105 110

aga tcc aag gag ttt gag gtg cag atg agt aca gca agt agt cct agc 385
Arg Ser Lys Glu Phe Glu Val Gln Met Ser Thr Ala Ser Ser Pro Ser
115 120 125

gaa atg gca caa gaa atg agc acg gga caa gtt gcc gaa ggg aga gat 433
Glu Met Ala Gln Glu Met Ser Thr Gly Gln Val Ala Glu Gly Arg Asp
130 135 140

gta cta cct ctt ttc cct atg gtt cca gta gaa cca gag agt gta cct 481
Val Leu Pro Leu Phe Pro Met Val Pro Val Glu Pro Glu Ser Val Pro
145 150 155 160

cat tct ctc gaa aca gga caa aaa act cga gtt atc aaa gtg 523
His Ser Leu Glu Thr Gly Gln Lys Thr Arg Val Ile Lys Val
165 170

<210> 43
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<212> PRT
<213> Pisum sativum

<400> 43

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20 25 30

Ile Pro Pro Pro Pro Glu Thr Pro Pro Gly Ser Gln Ala Tyr Phe Pro
35 40 45

Pro Tyr Gly Gly Met Pro Val Met Lys Ala Ala Ala Ser Glu Ser Ala
50 55 60

Val Glu His Val Asn Gln Phe Ser Ala Arg Gly Gln Ser Arg Arg Leu
65 70 75 80

Ser Glu Asp Glu Ala Asp Cys Asn Lys His Asn Gln Ser Ser Tyr Asp
85 90 95

Leu Pro Val Gln Arg Asn Gly Ala Thr Ser His Val Met Tyr His Gln
100 105 110

Arg Ser Lys Glu Phe Glu Val Gln Met Ser Thr Ala Ser Ser Pro Ser
115 120 125

Glu Met Ala Gln Glu Met Ser Thr Gly Gln Val Ala Glu Gly Arg Asp
130 135 140

Val Leu Pro Leu Phe Pro Met Val Pro Val Glu Pro Glu Ser Val Pro
145 150 155 160

His Ser Leu Glu Thr Gly Gln Lys Thr Arg Val Ile Lys Val
165 170

<210> 44
<211> 395
<212> DNA
<213> Glycine max

<220>
<221> Intron
<222> (1)..(301)
<223> partial

<220>
<221> exon
<222> (302)..(395)
<223> partial

<400> 44
ttatgtcttg ttaatatgtc gagtcctcct gaaaaaacca tgttaagatt tgtatgatga 60

tatgatataa attgtagaac ggaagatatt ccgcttaact gctaaccggt tttgtgatgt 120

gatcggagcc tctgattttg gtagttagtg gtttatatat cggtgcttcc atgttccaac 180

atgattatag atagctccaa acgcttaata tttccctttt atttcaactg tatatttctc 240

aagtcctaat aggacgagta ttgtgcaatt ttcttgatcc aactcctgtt cctctctaca 300

g tca aca gag agt gtt tgc tgt cca agt gtt tga gtt gca tag act gat 349
Ser Thr Glu Ser Val Cys Cys Pro Ser Val Val Ala Thr Asp
1 5 10

aaa ggt cca aca gct aat tgc tgg atc acc aga tat ttt gct tga a 395
Lys Gly Pro Thr Ala Asn Cys Trp Ile Thr Arg Tyr Phe Ala
15 20 25

<210> 45
<211> 31
<212> PRT
<213> Glycine max

<400> 45

Gln Gln Arg Val Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile
1 5 10 15

Lys Val Gln Gln Leu Ile Ala Gly Ser Pro Asp Ile Leu Leu Glu
20 25 30

<210> 46
<211> 477
<212> DNA
<213> Xanthium

<220>
<221> exon
<222> (2)..(13)
<223> partial

<220>
<221> exon
<222> (145)..(477)
<223> partial

<220>
<221> Intron
<222> (14)..(144)
<223> partial

<400> 46
t cga cta ata rag gtaaagcaac tccaaaggct gaatctcttg tagcaatttg 53
Arg Leu Ile Xaa
1

ggggggagggt gtgaaataga aaatatgatc tatatactgt ttttcgattc attactacgc 113

tgctcatgca tttttcctgt tattttaaca g gtc cag aag ctc att gcc gag 165
Val Gln Lys Leu Ile Ala Glu
5 10

tca cca aac agt atg ctt gaa gat gct gct tat tta ggc aaa cca tta 213
Ser Pro Asn Ser Met Leu Glu Asp Ala Ala Tyr Leu Gly Lys Pro Leu
15 20 25

aag agt tcg tct ggt aaa aga ctg cca ttg gag tgt att att aga gaa 261
Lys Ser Ser Ser Gly Lys Arg Leu Pro Leu Glu Cys Ile Ile Arg Glu
30 35 40

tct caa agt gtt ccg aag cgc aag aat gat tct gag aag cct aac ttc 309
Ser Gln Ser Val Pro Lys Arg Lys Asn Asp Ser Glu Lys Pro Asn Phe
45 50 55

agg atg gaa tgc tct gct gaa aac act gtg ggg aag gca tct ctt tct 357
Arg Met Glu Cys Ser Ala Glu Asn Thr Val Gly Lys Ala Ser Leu Ser
60 65 70 75

tct gtg caa aac agt agc cag ctc tct agc cac aga cca ttt tca gga 405
Ser Val Gln Asn Ser Ser Gln Leu Ser Ser His Arg Pro Phe Ser Gly
80 85 90

aat ccc cca cca acg cct gtg aca aac gat gct aac acg agt ccc tgg 453
Asn Pro Pro Pro Thr Pro Val Thr Asn Asp Ala Asn Thr Ser Pro Trp
95 100 105

tgc ttt caa caa cct ccg ggg cac 477
Cys Phe Gln Gln Pro Pro Gly His
110 115

<210> 47
<211> 115
<212> PRT
<213> Xanthium

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa = uncertain amino acid residue

<400> 47

Arg Leu Ile Xaa Val Gln Lys Leu Ile Ala Glu Ser Pro Asn Ser Met
1 5 10 15

```
Leu Glu Asp Ala Ala Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Gly
            20                  25                  30

Lys Arg Leu Pro Leu Glu Cys Ile Ile Arg Glu Ser Gln Ser Val Pro
        35                  40                  45

Lys Arg Lys Asn Asp Ser Glu Lys Pro Asn Phe Arg Met Glu Cys Ser
    50                  55                  60

Ala Glu Asn Thr Val Gly Lys Ala Ser Leu Ser Ser Val Gln Asn Ser
65                  70                  75                  80

Ser Gln Leu Ser Ser His Arg Pro Phe Ser Gly Asn Pro Pro Pro Thr
                85                  90                  95

Pro Val Thr Asn Asp Ala Asn Thr Ser Pro Trp Cys Phe Gln Gln Pro
            100                 105                 110

Pro Gly His
        115


<210>  48
<211>  433
<212>  DNA
<213>  Xanthium

<220>
<221>  exon
<222>  (2)..(13)
<223>  partial


<220>
<221>  exon
<222>  (128)..(433)
<223>  partial


<220>
<221>  Intron
<222>  (14)..(127)
<223>  partial


<400>  48
t mga cta ctc rag gtaaagcaac tgtagagact gaataacttc aattatcagc        53
  Xaa Leu Leu Xaa
  1
```

```
tttgagattt tgcattccct gtttttcctt ggacttggta ttttgctcaa atttttctgt    113

ttgttactca ttag gtc cag aaa ctg ata gct agt tcg cca aat agt ata      163
               Val Gln Lys Leu Ile Ala Ser Ser Pro Asn Ser Ile
               5                   10                  15

ctc gaa gat ggt tct tct tta ggc aaa cct tta aag agg ttg tct act      211
Leu Glu Asp Gly Ser Ser Leu Gly Lys Pro Leu Lys Arg Leu Ser Thr
            20                  25                  30

aaa aga ctt gca ttg gag tat aat gtc aaa gca cct gaa aat gtt tcg      259
Lys Arg Leu Ala Leu Glu Tyr Asn Val Lys Ala Pro Glu Asn Val Ser
        35                  40                  45

aaa cag aag aat gat tct gag aag cct aac tct agg atg gaa tcc aat      307
Lys Gln Lys Asn Asp Ser Glu Lys Pro Asn Ser Arg Met Glu Ser Asn
    50                  55                  60

gcc gaa aat gat gta gga gag aca tct ctt tct tgc cgc aga cca ctt      355
Ala Glu Asn Asp Val Gly Glu Thr Ser Leu Ser Cys Arg Arg Pro Leu
65                  70                  75                  80

tca gaa acc ccg tca cca aca cca gta aaa cac gtt tcc cac atg ggt      403
Ser Glu Thr Pro Ser Pro Thr Pro Val Lys His Val Ser His Met Gly
               85                  90                  95

ccg tgg ctc ttc aat caa cct tcg gga cac                             433
Pro Trp Leu Phe Asn Gln Pro Ser Gly His
            100                 105
```

<210> 49
<211> 106
<212> PRT
<213> Xanthium

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa = uncertain amino acid residue

<400> 49

```
Arg Leu Leu Xaa Val Gln Lys Leu Ile Ala Ser Ser Pro Asn Ser Ile
1               5                   10                  15

Leu Glu Asp Gly Ser Ser Leu Gly Lys Pro Leu Lys Arg Leu Ser Thr
            20                  25                  30

Lys Arg Leu Ala Leu Glu Tyr Asn Val Lys Ala Pro Glu Asn Val Ser
        35                  40                  45
```

```
Lys Gln Lys Asn Asp Ser Glu Lys Pro Asn Ser Arg Met Glu Ser Asn
    50                  55                  60

Ala Glu Asn Asp Val Gly Glu Thr Ser Leu Ser Cys Arg Arg Pro Leu
65                  70                  75                  80

Ser Glu Thr Pro Ser Pro Thr Pro Val Lys His Val Ser His Met Gly
                85                  90                  95

Pro Trp Leu Phe Asn Gln Pro Ser Gly His
            100                 105
```

<210> 50
<211> 526
<212> DNA
<213> Xanthium

<220>
<221> exon
<222> (2)..(526)
<223> partial

<400> 50

```
a cat cct gga cct gca ttc atg agt cca gta tat ggc ggt tgt gga ccc     49
  His Pro Gly Pro Ala Phe Met Ser Pro Val Tyr Gly Gly Cys Gly Pro
  1               5                  10                  15

ccg att cca atg acg gga aac ttt tta gct ccg gca tac tat caa gga      97
Pro Ile Pro Met Thr Gly Asn Phe Leu Ala Pro Ala Tyr Tyr Gln Gly
            20                  25                  30

acg gga gct cct ttc gca cct caa cct agt cat ggc tac ttt cct ccg     145
Thr Gly Ala Pro Phe Ala Pro Gln Pro Ser His Gly Tyr Phe Pro Pro
        35                  40                  45

ttt gac atg cca gtt atg aat cca gta atc cca tct cca gct att gat     193
Phe Asp Met Pro Val Met Asn Pro Val Ile Pro Ser Pro Ala Ile Asp
    50                  55                  60

caa ccg gac cag gtt gct gca acg ggt ttt caa ggt ctg tta tcg aga     241
Gln Pro Asp Gln Val Ala Ala Thr Gly Phe Gln Gly Leu Leu Ser Arg
65                  70                  75                  80

gat cag gaa gtt aat ttt cac att caa caa cag aac tca agt aat gtt     289
Asp Gln Glu Val Asn Phe His Ile Gln Gln Gln Asn Ser Ser Asn Val
                85                  90                  95

gcg aga gag aat aat gta gcc gcg cca aag gtt gtg aga ttg tat ccc     337
Ala Arg Glu Asn Asn Val Ala Ala Pro Lys Val Val Arg Leu Tyr Pro
            100                 105                 110

tct aga gat tct gag ttg caa gcc agc act gca agt agt cca agg gaa     385
```

```
Ser Arg Asp Ser Glu Leu Gln Ala Ser Thr Ala Ser Ser Pro Arg Glu
        115                 120                 125

aga ggt cat gga tta gac gtg ggc aac tcc acc gga gga aga agc gtg      433
Arg Gly His Gly Leu Asp Val Gly Asn Ser Thr Gly Gly Arg Ser Val
    130                 135                 140

ttt cct ctg ttc cca act ttt cct gct att agc aac ccc gct agt agc      481
Phe Pro Leu Phe Pro Thr Phe Pro Ala Ile Ser Asn Pro Ala Ser Ser
145                 150                 155                 160

tcc cag cct cat ttt cct agt cat acg gct aga gtt atc aaa gtt          526
Ser Gln Pro His Phe Pro Ser His Thr Ala Arg Val Ile Lys Val
                165                 170                 175
```

<210> 51
<211> 175
<212> PRT
<213> Xanthium

<400> 51

```
His Pro Gly Pro Ala Phe Met Ser Pro Val Tyr Gly Gly Cys Gly Pro
1               5                   10                  15

Pro Ile Pro Met Thr Gly Asn Phe Leu Ala Pro Ala Tyr Tyr Gln Gly
            20                  25                  30

Thr Gly Ala Pro Phe Ala Pro Gln Pro Ser His Gly Tyr Phe Pro Pro
        35                  40                  45

Phe Asp Met Pro Val Met Asn Pro Val Ile Pro Ser Pro Ala Ile Asp
    50                  55                  60

Gln Pro Asp Gln Val Ala Ala Thr Gly Phe Gln Gly Leu Leu Ser Arg
65                  70                  75                  80

Asp Gln Glu Val Asn Phe His Ile Gln Gln Gln Asn Ser Ser Asn Val
                85                  90                  95

Ala Arg Glu Asn Asn Val Ala Ala Pro Lys Val Val Arg Leu Tyr Pro
            100                 105                 110

Ser Arg Asp Ser Glu Leu Gln Ala Ser Thr Ala Ser Ser Pro Arg Glu
        115                 120                 125

Arg Gly His Gly Leu Asp Val Gly Asn Ser Thr Gly Gly Arg Ser Val
    130                 135                 140
```

```
Phe Pro Leu Phe Pro Thr Phe Pro Ala Ile Ser Asn Pro Ala Ser Ser
145                 150                 155                 160


Ser Gln Pro His Phe Pro Ser His Thr Ala Arg Val Ile Lys Val
                165                 170                 175


<210>  52
<211>  532
<212>  DNA
<213>  poplar trees

<220>
<221>  exon
<222>  (2)..(532)
<223>  partial


<400>  52
t tac act gcc cck gga ttc atg gga tcg ggt tgt gga gga tgt gga cct     49
  Tyr Thr Ala Xaa Gly Phe Met Gly Ser Gly Cys Gly Gly Cys Gly Pro
  1               5                   10                  15

ttt ggg cca att ccc ttg aca gac aac ttt atg act tca gct tat gcg      97
Phe Gly Pro Ile Pro Leu Thr Asp Asn Phe Met Thr Ser Ala Tyr Ala
            20                  25                  30

att cca aca tct cat tat cat caa ggt att ggg gtc tca cca ggt gct     145
Ile Pro Thr Ser His Tyr His Gln Gly Ile Gly Val Ser Pro Gly Ala
        35                  40                  45

cct cca gtt ggt aat gct tgc ttc gcc cca tat ggc atg cca gga atg     193
Pro Pro Val Gly Asn Ala Cys Phe Ala Pro Tyr Gly Met Pro Gly Met
    50                  55                  60

aac cca gcc atc tca ggt tct gca ggg tct ggt tcc tgt ggt caa act     241
Asn Pro Ala Ile Ser Gly Ser Ala Gly Ser Gly Ser Cys Gly Gln Thr
65                  70                  75                  80

gct cag ttt cca gga ggc att ttg agc tcg aac atg cca cat caa agc     289
Ala Gln Phe Pro Gly Gly Ile Leu Ser Ser Asn Met Pro His Gln Ser
                85                  90                  95

tca tgt aat gaa cgg act caa aag agt gaa gct gtt tta gaa ggt atg     337
Ser Cys Asn Glu Arg Thr Gln Lys Ser Glu Ala Val Leu Glu Gly Met
            100                 105                 110

aag ctt cgg gca tct aaa aac act tcg gta caa gga agt aca ggt agt     385
Lys Leu Arg Ala Ser Lys Asn Thr Ser Val Gln Gly Ser Thr Gly Ser
        115                 120                 125

agt ccc agt ggc aga gtg caa ggg gtt ggg act gtt caa gcc gct gat     433
Ser Pro Ser Gly Arg Val Gln Gly Val Gly Thr Val Gln Ala Ala Asp
    130                 135                 140
```

```
gga aga gct gcg ttc cca cct ttc cca gtg act cct cct tgc cct gag      481
Gly Arg Ala Ala Phe Pro Pro Phe Pro Val Thr Pro Pro Cys Pro Glu
145                 150                 155                 160

gga gcc cct cag cat caa gag aca gac cag ctg tcg aaa gtg atc aag      529
Gly Ala Pro Gln His Gln Glu Thr Asp Gln Leu Ser Lys Val Ile Lys
                165                 170                 175

gtt                                                                  532
Val
```

<210> 53
<211> 177
<212> PRT
<213> Poplar trees

<220>
<221> misc_feature
<222> (4)..(4)
<223> Xaa = uncertain amino acid residue

<400> 53

```
Tyr Thr Ala Xaa Gly Phe Met Gly Ser Gly Cys Gly Gly Cys Gly Pro
1               5                   10                  15

Phe Gly Pro Ile Pro Leu Thr Asp Asn Phe Met Thr Ser Ala Tyr Ala
            20                  25                  30

Ile Pro Thr Ser His Tyr His Gln Gly Ile Gly Val Ser Pro Gly Ala
        35                  40                  45

Pro Pro Val Gly Asn Ala Cys Phe Ala Pro Tyr Gly Met Pro Gly Met
    50                  55                  60

Asn Pro Ala Ile Ser Gly Ser Ala Gly Ser Gly Ser Cys Gly Gln Thr
65                  70                  75                  80

Ala Gln Phe Pro Gly Gly Ile Leu Ser Ser Asn Met Pro His Gln Ser
                85                  90                  95

Ser Cys Asn Glu Arg Thr Gln Lys Ser Glu Ala Val Leu Glu Gly Met
            100                 105                 110

Lys Leu Arg Ala Ser Lys Asn Thr Ser Val Gln Gly Ser Thr Gly Ser
        115                 120                 125
```

```
Ser Pro Ser Gly Arg Val Gln Gly Val Gly Thr Val Gln Ala Ala Asp
    130                 135                 140

Gly Arg Ala Ala Phe Pro Pro Phe Pro Val Thr Pro Pro Cys Pro Glu
145                 150                 155                 160

Gly Ala Pro Gln His Gln Glu Thr Asp Gln Leu Ser Lys Val Ile Lys
                165                 170                 175

Val
```

<210> 54
<211> 418
<212> DNA
<213> Mimulus sp.

<220>
<221> exon
<222> (2)..(418)
<223>

<400> 54

```
g tac ccg ttc gtc agc caa ccc tgt gga ggg ggc tgc ggc ccc cct gga     49
  Tyr Pro Phe Val Ser Gln Pro Cys Gly Gly Gly Cys Gly Pro Pro Gly
  1               5                  10                  15

tcg aat cca acg gtg gga aat ttc tca act cca cca ccg cca caa tat      97
Ser Asn Pro Thr Val Gly Asn Phe Ser Thr Pro Pro Pro Pro Gln Tyr
            20                  25                  30

cat cat tta cct tct ttc cct cag ttc ccc ccc cac ggc tac ttc cct     145
His His Leu Pro Ser Phe Pro Gln Phe Pro Pro His Gly Tyr Phe Pro
        35                  40                  45

cct tac tgt gtc ccg att atg gac acg tca gca ttc tcg ggc ccg ccc     193
Pro Tyr Cys Val Pro Ile Met Asp Thr Ser Ala Phe Ser Gly Pro Pro
    50                  55                  60

ccc gaa cag acc ata cga gcc cca gct gct gca ggc cca gct gta caa     241
Pro Glu Gln Thr Ile Arg Ala Pro Ala Ala Ala Gly Pro Ala Val Gln
65                  70                  75                  80

aaa agc ggg ccc gct tta tgg gat gtc gaa atg caa ggg agc aca gct     289
Lys Ser Gly Pro Ala Leu Trp Asp Val Glu Met Gln Gly Ser Thr Ala
                85                  90                  95

agt agc ccg agt ggg agg cgt aaa aga gga agc aac ggt gtt gaa ttt     337
Ser Ser Pro Ser Gly Arg Arg Lys Arg Gly Ser Asn Gly Val Glu Phe
            100                 105                 110
```

```
gaa aga agg aat atg ctt ccg ctt ttc ccc act acc cca gct gct gtg      385
Glu Arg Arg Asn Met Leu Pro Leu Phe Pro Thr Thr Pro Ala Ala Val
        115                 120                 125

gat gcc ttg aaa cca acg cgg gtg att aag gtt                        418
Asp Ala Leu Lys Pro Thr Arg Val Ile Lys Val
    130                 135
```

<210> 55
<211> 139
<212> PRT
<213> Mimulus sp.

<400> 55

```
Tyr Pro Phe Val Ser Gln Pro Cys Gly Gly Gly Cys Gly Pro Pro Gly
1               5                   10                  15

Ser Asn Pro Thr Val Gly Asn Phe Ser Thr Pro Pro Pro Pro Gln Tyr
            20                  25                  30

His His Leu Pro Ser Phe Pro Gln Phe Pro Pro His Gly Tyr Phe Pro
        35                  40                  45

Pro Tyr Cys Val Pro Ile Met Asp Thr Ser Ala Phe Ser Gly Pro Pro
    50                  55                  60

Pro Glu Gln Thr Ile Arg Ala Pro Ala Ala Ala Gly Pro Ala Val Gln
65                  70                  75                  80

Lys Ser Gly Pro Ala Leu Trp Asp Val Glu Met Gln Gly Ser Thr Ala
                85                  90                  95

Ser Ser Pro Ser Gly Arg Arg Lys Arg Gly Ser Asn Gly Val Glu Phe
            100                 105                 110

Glu Arg Arg Asn Met Leu Pro Leu Phe Pro Thr Thr Pro Ala Ala Val
        115                 120                 125

Asp Ala Leu Lys Pro Thr Arg Val Ile Lys Val
    130                 135
```

<210> 56
<211> 1272
<212> DNA
<213> Zea mays

<220>
<221> exon
<222> (3)..(185)
<223> partial

<220>
<221> Intron
<222> (186)..(295)
<223>

<220>
<221> exon
<222> (296)..(1066)
<223>

<220>
<221> 3'UTR
<222> (1067)..(1272)
<223>

<400> 56

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at gac gtg gag caa aac gat gat ctg tct gat tcc tct gtt gaa tct        47
   Asp Val Glu Gln Asn Asp Asp Leu Ser Asp Ser Ser Val Glu Ser
   1               5                  10                  15

ttg cct gga atg gag att tct cca gat gat gtt gtc agt gct att ggt       95
Leu Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly
                20                  25                  30

ccc aag cat ttt tgg aaa gcg aga aga gct att gtc aat cag cag agg      143
Pro Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg
            35                  40                  45

gta ttt gct gtt caa gta ttc gag ctg cat agg ttg atc aaa             185
Val Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys
        50                  55                  60

gtgagtctgc ggcaaataaa tataacttct ttgggcccat gcttatgggc aggttaattt    245

aaatttgaaa awttggttta acsgttgttt atgttgactt ttgcaatcag gtg cag       301
                                                        Val Gln

aag ttg atc gct gca tct cca cat gta ctt att gag ggg gat cct tgc      349
Lys Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys
    65                  70                  75

ctt ggc aaa tcc ttg gcg gtg agc aag aaa agg ctg gct gga gat gtg      397
Leu Gly Lys Ser Leu Ala Val Ser Lys Lys Arg Leu Ala Gly Asp Val
80                  85                  90                  95

gaa aca cag ctt gaa tca gct aaa aac gat gat ggc gtg cga cca acg      445
```

```
Glu Thr Gln Leu Glu Ser Ala Lys Asn Asp Asp Gly Val Arg Pro Thr
                100                 105                 110

cag cta gag cac tcg aaa gag aag act gaa gcg aac caa cct tca cca      493
Gln Leu Glu His Ser Lys Glu Lys Thr Glu Ala Asn Gln Pro Ser Pro
            115                 120                 125

tct caa gac gaa cag gcc gca act aat ggt gac gtt gct gcc ttg atg      541
Ser Gln Asp Glu Gln Ala Ala Thr Asn Gly Asp Val Ala Ala Leu Met
        130                 135                 140

cat acc cct tcc gac aac aaa cag aag agc tgg tgc att cct gca cct      589
His Thr Pro Ser Asp Asn Lys Gln Lys Ser Trp Cys Ile Pro Ala Pro
    145                 150                 155

cca agt cag tgg ctg att cct gtw atg tcc ccg tct gaa gga ctt gtc      637
Pro Ser Gln Trp Leu Ile Pro Xaa Met Ser Pro Ser Glu Gly Leu Val
160                 165                 170                 175

tac aag cct tat acc ggg cac tgc cct ccg gtg gga agt ctt ttg gcg      685
Tyr Lys Pro Tyr Thr Gly His Cys Pro Pro Val Gly Ser Leu Leu Ala
                180                 185                 190

ccc cca ttt ttt gcc agc tac ccc acc tcc tcc tcc tcc aca gct ggg      733
Pro Pro Phe Phe Ala Ser Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly
            195                 200                 205

ggg gat ttc atg agt tcg gca tgt gga gcc agg ctg atg agt gcc cct      781
Gly Asp Phe Met Ser Ser Ala Cys Gly Ala Arg Leu Met Ser Ala Pro
        210                 215                 220

gtg tac ttc ccg tct ttc agc atg cct gca gtg tca ggg tct gca gtt      829
Val Tyr Phe Pro Ser Phe Ser Met Pro Ala Val Ser Gly Ser Ala Val
    225                 230                 235

gag caa gtg agc cat gtt gca gcg tcg cag cat aaa cgg aac tcg tgt      877
Glu Gln Val Ser His Val Ala Ala Ser Gln His Lys Arg Asn Ser Cys
240                 245                 250                 255

agt gaa gcg gtg ttg gca tca agg gac agc gag gtg caa ggc agt agt      925
Ser Glu Ala Val Leu Ala Ser Arg Asp Ser Glu Val Gln Gly Ser Ser
                260                 265                 270

gct agc agt ccg gca tct tct gaa aca gca gct caa ccc agg gtc att      973
Ala Ser Ser Pro Ala Ser Ser Glu Thr Ala Ala Gln Pro Arg Val Ile
            275                 280                 285

agg gtt gtt ccc cac acg gca cgc acg gct tca gag tcg gca gca agg     1021
Arg Val Val Pro His Thr Ala Arg Thr Ala Ser Glu Ser Ala Ala Arg
        290                 295                 300

att ttc cgc tca ata cag atg gag agg aaa caa aac gac ccg tga         1066
Ile Phe Arg Ser Ile Gln Met Glu Arg Lys Gln Asn Asp Pro
    305                 310                 315

ctggcagata aaaatgaaag aacggaggga gtagactaat tttttgaccg ataattataa   1126
```

tgatcgccgt aaattggctg gcccgcccgc cttatgtttt ttgttcagtg taaatatgct 1186

gtgtctgtca gaatgatatg gcatctgtag ctattttggt tctgtcagaa tcatgttgat 1246

tggaattaaa aaaaaaaaaa aaaaaa 1272

<210> 57
<211> 317
<212> PRT
<213> Zea mays

<400> 57

Asp Val Glu Gln Asn Asp Asp Leu Ser Asp Ser Ser Val Glu Ser Leu
1 5 10 15

Pro Gly Met Glu Ile Ser Pro Asp Asp Val Val Ser Ala Ile Gly Pro
20 25 30

Lys His Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln Arg Val
35 40 45

Phe Ala Val Gln Val Phe Glu Leu His Arg Leu Ile Lys Val Gln Lys
50 55 60

Leu Ile Ala Ala Ser Pro His Val Leu Ile Glu Gly Asp Pro Cys Leu
65 70 75 80

Gly Lys Ser Leu Ala Val Ser Lys Lys Arg Leu Ala Gly Asp Val Glu
85 90 95

Thr Gln Leu Glu Ser Ala Lys Asn Asp Asp Gly Val Arg Pro Thr Gln
100 105 110

Leu Glu His Ser Lys Glu Lys Thr Glu Ala Asn Gln Pro Ser Pro Ser
115 120 125

Gln Asp Glu Gln Ala Ala Thr Asn Gly Asp Val Ala Ala Leu Met His
130 135 140

Thr Pro Ser Asp Asn Lys Gln Lys Ser Trp Cys Ile Pro Ala Pro Pro
145 150 155 160

Ser Gln Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr
165 170 175

```
Lys Pro Tyr Thr Gly His Cys Pro Pro Val Gly Ser Leu Leu Ala Pro
            180                 185                 190

Pro Phe Phe Ala Ser Tyr Pro Thr Ser Ser Ser Ser Thr Ala Gly Gly
        195                 200                 205

Asp Phe Met Ser Ser Ala Cys Gly Ala Arg Leu Met Ser Ala Pro Val
    210                 215                 220

Tyr Phe Pro Ser Phe Ser Met Pro Ala Val Ser Gly Ser Ala Val Glu
225                 230                 235                 240

Gln Val Ser His Val Ala Ala Ser Gln His Lys Arg Asn Ser Cys Ser
                245                 250                 255

Glu Ala Val Leu Ala Ser Arg Asp Ser Glu Val Gln Gly Ser Ser Ala
            260                 265                 270

Ser Ser Pro Ala Ser Ser Glu Thr Ala Ala Gln Pro Arg Val Ile Arg
        275                 280                 285

Val Val Pro His Thr Ala Arg Thr Ala Ser Glu Ser Ala Ala Arg Ile
    290                 295                 300

Phe Arg Ser Ile Gln Met Glu Arg Lys Gln Asn Asp Pro
305                 310                 315
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<210> 58
<211> 1980
<212> DNA
<213> Lycopersicon esculentum

<220>
<221> exon
<222> (2)..(1804)
<223> portion of exon 1, exon 2, exon 3, and exon 4, including stop cod
on

<220>
<221> 3'UTR
<222> (1085)..(1980)
<223> partial

<400> 58
g cct tct cag aga ttc aac tct ggg gtt ttg cct ctt gat cct aac aat 49

```
  Pro Ser Gln Arg Phe Asn Ser Gly Val Leu Pro Leu Asp Pro Asn Asn
  1               5                  10                  15

act tca aag atg gcc cct cca tcc tca agc cag ggg agt ggg cat gac      97
Thr Ser Lys Met Ala Pro Pro Ser Ser Ser Gln Gly Ser Gly His Asp
            20                  25                  30

aga agt gga tat ctc cct ata caa cac cct cca tct aga cgt cta gct     145
Arg Ser Gly Tyr Leu Pro Ile Gln His Pro Pro Ser Arg Arg Leu Ala
        35                  40                  45

gat aaa cca cct ggc cac agt tcc gat ccc agt act ctc ttg caa caa     193
Asp Lys Pro Pro Gly His Ser Ser Asp Pro Ser Thr Leu Leu Gln Gln
    50                  55                  60

tat gaa ttg aaa aag aga aca gaa gag gat gac ttt acg gtc ccc atc     241
Tyr Glu Leu Lys Lys Arg Thr Glu Glu Asp Asp Phe Thr Val Pro Ile
65                  70                  75                  80

ttt gtt aat tcc aag ctc ggt cag gcc cat ggg agt cat aat gtg aat     289
Phe Val Asn Ser Lys Leu Gly Gln Ala His Gly Ser His Asn Val Asn
                85                  90                  95

atg gaa aag ctc tca ccc tct ggt caa ctg ttt tgt cct aat aaa gag     337
Met Glu Lys Leu Ser Pro Ser Gly Gln Leu Phe Cys Pro Asn Lys Glu
            100                 105                 110

ttg gaa gga gtt aca cat cta aca ttg aga caa cag cgc aat agc caa     385
Leu Glu Gly Val Thr His Leu Thr Leu Arg Gln Gln Arg Asn Ser Gln
        115                 120                 125

aac aag gag aat ctc aaa tgt act ctt gct cgt aga gag aaa aca acc     433
Asn Lys Glu Asn Leu Lys Cys Thr Leu Ala Arg Arg Glu Lys Thr Thr
    130                 135                 140

tca aac tct gca tcc aag gaa tgc aga ttg gat cct cag gtt ggt tgt     481
Ser Asn Ser Ala Ser Lys Glu Cys Arg Leu Asp Pro Gln Val Gly Cys
145                 150                 155                 160

agt agc ata cct gaa cct gtt aag gga aca tat gat ggc agt tcg tat     529
Ser Ser Ile Pro Glu Pro Val Lys Gly Thr Tyr Asp Gly Ser Ser Tyr
                165                 170                 175

cct agg aaa gaa ttt gta tca taa gag cag tta act gct aat gat ctt     577
Pro Arg Lys Glu Phe Val Ser     Glu Gln Leu Thr Ala Asn Asp Leu
            180                 185                 190

gtt aat gat acg gaa tcc cag gaa gac agg gca cac aaa tca tta caa     625
Val Asn Asp Thr Glu Ser Gln Glu Asp Arg Ala His Lys Ser Leu Gln
            195                 200                 205

aca gga aat ttg gac cga ggt gac gac tta tct gag act tcc aga gtg     673
Thr Gly Asn Leu Asp Arg Gly Asp Asp Leu Ser Glu Thr Ser Arg Val
        210                 215                 220

gaa tct att tct gga aca gac atc tct cct gat gac att gta gga ata     721
Glu Ser Ile Ser Gly Thr Asp Ile Ser Pro Asp Asp Ile Val Gly Ile
```

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    225                 230                 235

att ggc tta aag cgt ttc tgg aaa gcc aga aga gca att gtc aac cag      769
Ile Gly Leu Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln
240                 245                 250                 255

caa aga gtg ttt gca atc caa gtg ttc gag ttg cat cga cta ata aag      817
Gln Arg Val Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys
                260                 265                 270

gta caa agg ctc att gcc ggg tca cca aat agt tcg ctc gaa gat cct      865
Val Gln Arg Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro
            275                 280                 285

gct tat tta ggc aaa cct tta aag agt tca tcg atc aaa aga ctt cca      913
Ala Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro
        290                 295                 300

ttg gac tgt att gtt aga gaa tct caa agt gtt ctg aag cgc aag cat      961
Leu Asp Cys Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His
    305                 310                 315

gat tct gag aag cct cac ttc agg atg gaa cac act gcc gaa agc aat     1009
Asp Ser Glu Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn
320                 325                 330                 335

gtg gga aag gca tct ctc tct act gtg caa aat ggt agt caa ctc tct     1057
Val Gly Lys Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser
                340                 345                 350

agc cac aaa cca ttt tca gga act cca ctg cct aca cct gta aca aat     1105
Ser His Lys Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn
            355                 360                 365

gat tct aat gcg ggt cct tgg tgc ttc caa caa cct ccc ggg cac caa     1153
Asp Ser Asn Ala Gly Pro Trp Cys Phe Gln Gln Pro Pro Gly His Gln
        370                 375                 380

tgg ttg atc cca gtg atg tct cct tct gag gga ctt gta tac aag cca     1201
Trp Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro
    385                 390                 395

ttt cct gga cct gga ttc acg agt cct att tgt gga agt ggg cct cca     1249
Phe Pro Gly Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Pro
400                 405                 410                 415

gga tcg agt cca aca atg ggg aac ttt ttt gct cca aca tat gga gtt     1297
Gly Ser Ser Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val
                420                 425                 430

cct gct cct aat cct cac tat caa ggt atg gga gtt cct ttt gca cct     1345
Pro Ala Pro Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro
            435                 440                 445

ccg act ggt cat ggt tac ttt cgg caa tat ggc atg cca gct atg aat     1393
Pro Thr Gly His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn
        450                 455                 460
```

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cca cca att tca tca act gct agt gaa gaa tcg aac cag tat acc atg     1441
Pro Pro Ile Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met
    465                 470                 475

cct ggt tta caa cac cag ttt tct gga gta gtt gat gac gtc aac att     1489
Pro Gly Leu Gln His Gln Phe Ser Gly Val Val Asp Asp Val Asn Ile
480                 485                 490                 495

caa cat cag gac tca agt aat gtt cta aat cag aag aaa gaa aat gtc     1537
Gln His Gln Asp Ser Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val
                500                 505                 510

ccg gat gtt gta agg tat caa tcc aca aaa gat aat gag gta caa gcc     1585
Pro Asp Val Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala
            515                 520                 525

agc agt gca agt agt cct att gag aca gca gga aga aac atg ctc tct     1633
Ser Ser Ala Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser
        530                 535                 540

ctt ttt ccc acg tct cca gtt act gac aac cgt gat ggt agc cct cag     1681
Leu Phe Pro Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln
    545                 550                 555

gct tgt gtg cct gat aat cca gcc aga gtt atc aag gtt gta cct cac     1729
Ala Cys Val Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His
560                 565                 570                 575

aat gca agg tct gct aca gaa tcc gta gct cgg ata ttt cag tct ata     1777
Asn Ala Arg Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile
                580                 585                 590

caa caa gag aga aat aat atg act tag gtttaacaca tctataagta           1824
Gln Gln Glu Arg Asn Asn Met Thr
            595

gcttaccttg tgaatatgac catttgctca tcctggcaaa atgtagtagt ttcagtcaat   1884

ttgttgtatc tttcttttct acagaaagta tgtaatagct gtattttaat ttggttgctg   1944

tagataagca tacctgcaaa aaaaaaaaaa aaaaac                             1980
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<210> 59
<211> 599
<212> PRT
<213> Lycopersicum esculentum

<400> 59

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Pro Ser Gln Arg Phe Asn Ser Gly Val Leu Pro Leu Asp Pro Asn Asn
1               5                   10                  15

Thr Ser Lys Met Ala Pro Pro Ser Ser Ser Gln Gly Ser Gly His Asp
            20                  25                  30
```

```
Arg Ser Gly Tyr Leu Pro Ile Gln His Pro Pro Ser Arg Arg Leu Ala
        35                  40                  45

Asp Lys Pro Pro Gly His Ser Ser Asp Pro Ser Thr Leu Leu Gln Gln
    50                  55                  60

Tyr Glu Leu Lys Lys Arg Thr Glu Glu Asp Asp Phe Thr Val Pro Ile
65                  70                  75                  80

Phe Val Asn Ser Lys Leu Gly Gln Ala His Gly Ser His Asn Val Asn
                85                  90                  95

Met Glu Lys Leu Ser Pro Ser Gly Gln Leu Phe Cys Pro Asn Lys Glu
            100                 105                 110

Leu Glu Gly Val Thr His Leu Thr Leu Arg Gln Gln Arg Asn Ser Gln
        115                 120                 125

Asn Lys Glu Asn Leu Lys Cys Thr Leu Ala Arg Arg Glu Lys Thr Thr
    130                 135                 140

Ser Asn Ser Ala Ser Lys Glu Cys Arg Leu Asp Pro Gln Val Gly Cys
145                 150                 155                 160

Ser Ser Ile Pro Glu Pro Val Lys Gly Thr Tyr Asp Gly Ser Ser Tyr
                165                 170                 175

Pro Arg Lys Glu Phe Val Ser Glu Gln Leu Thr Ala Asn Asp Leu Val
            180                 185                 190

Asn Asp Thr Glu Ser Gln Glu Asp Arg Ala His Lys Ser Leu Gln Thr
        195                 200                 205

Gly Asn Leu Asp Arg Gly Asp Asp Leu Ser Glu Thr Ser Arg Val Glu
    210                 215                 220

Ser Ile Ser Gly Thr Asp Ile Ser Pro Asp Asp Ile Val Gly Ile Ile
225                 230                 235                 240

Gly Leu Lys Arg Phe Trp Lys Ala Arg Arg Ala Ile Val Asn Gln Gln
                245                 250                 255
```

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Arg Val Phe Ala Ile Gln Val Phe Glu Leu His Arg Leu Ile Lys Val
            260                 265                 270

Gln Arg Leu Ile Ala Gly Ser Pro Asn Ser Ser Leu Glu Asp Pro Ala
        275                 280                 285

Tyr Leu Gly Lys Pro Leu Lys Ser Ser Ser Ile Lys Arg Leu Pro Leu
    290                 295                 300

Asp Cys Ile Val Arg Glu Ser Gln Ser Val Leu Lys Arg Lys His Asp
305                 310                 315                 320

Ser Glu Lys Pro His Phe Arg Met Glu His Thr Ala Glu Ser Asn Val
                325                 330                 335

Gly Lys Ala Ser Leu Ser Thr Val Gln Asn Gly Ser Gln Leu Ser Ser
            340                 345                 350

His Lys Pro Phe Ser Gly Thr Pro Leu Pro Thr Pro Val Thr Asn Asp
        355                 360                 365

Ser Asn Ala Gly Pro Trp Cys Phe Gln Gln Pro Pro Gly His Gln Trp
    370                 375                 380

Leu Ile Pro Val Met Ser Pro Ser Glu Gly Leu Val Tyr Lys Pro Phe
385                 390                 395                 400

Pro Gly Pro Gly Phe Thr Ser Pro Ile Cys Gly Ser Gly Pro Pro Gly
                405                 410                 415

Ser Ser Pro Thr Met Gly Asn Phe Phe Ala Pro Thr Tyr Gly Val Pro
            420                 425                 430

Ala Pro Asn Pro His Tyr Gln Gly Met Gly Val Pro Phe Ala Pro Pro
        435                 440                 445

Thr Gly His Gly Tyr Phe Arg Gln Tyr Gly Met Pro Ala Met Asn Pro
    450                 455                 460

Pro Ile Ser Ser Thr Ala Ser Glu Glu Ser Asn Gln Tyr Thr Met Pro
465                 470                 475                 480
```

```
Gly Leu Gln His Gln Phe Ser Gly Val Val Asp Asp Val Asn Ile Gln
                485                 490                 495

His Gln Asp Ser Ser Asn Val Leu Asn Gln Lys Lys Glu Asn Val Pro
            500                 505                 510

Asp Val Val Arg Tyr Gln Ser Thr Lys Asp Asn Glu Val Gln Ala Ser
        515                 520                 525

Ser Ala Ser Ser Pro Ile Glu Thr Ala Gly Arg Asn Met Leu Ser Leu
    530                 535                 540

Phe Pro Thr Ser Pro Val Thr Asp Asn Arg Asp Gly Ser Pro Gln Ala
545                 550                 555                 560

Cys Val Pro Asp Asn Pro Ala Arg Val Ile Lys Val Val Pro His Asn
                565                 570                 575

Ala Arg Ser Ala Thr Glu Ser Val Ala Arg Ile Phe Gln Ser Ile Gln
            580                 585                 590

Gln Glu Arg Asn Asn Met Thr
        595
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<210> 60
<211> 1972
<212> DNA
<213> Brassica sp.

<220>
<221> exon
<222> (1)..(147)
<223> partial

<220>
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<222> (344)..(792)
<223>

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<222> (1505)..(1556)
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<222> (1649)..(1972)
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<222> (148)..(343)
<223>

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<221> Intron
<222> (793)..(1504)
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<220>
<221> Intron
<222> (1557)..(1648)
<223>

<400> 60

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aaa gga gga gga cct cga gct cct cct aga aac aag atg gct ctc tac       48
Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu Tyr
1               5                   10                  15

gag cac ctc acc acc cct tct cac agg ttt act gat cat agt tcc tcg       96
Glu His Leu Thr Thr Pro Ser His Arg Phe Thr Asp His Ser Ser Ser
            20                  25                  30

cca cgt cac acc aac act ctc ttt cct cct cct cct gga cca tct aac      144
Pro Arg His Thr Asn Thr Leu Phe Pro Pro Pro Pro Gly Pro Ser Asn
        35                  40                  45

cag gtactactga gtttttagta ataatatata ttagttacag caaatcttaa           197
Gln

tttcttgctg tgtcttatta ccatgtttcg tttgtggaaa tgattatctt ttaaagctat    257

aaccttcttg ttatgctgaa tagtttcagt agaagattat atagtgtatg tgggacattg    317

gaaataatta tctttttatt ctgcag cct tgt ggg gtg gag aga aac ttg act     370
                            Pro Cys Gly Val Glu Arg Asn Leu Thr
                            50                  55

tcc cag cat ctt gat tct tca gct tct ggc cat gta acc caa atg tcc      418
Ser Gln His Leu Asp Ser Ser Ala Ser Gly His Val Thr Gln Met Ser
    60                  65                  70

tcc atg gaa aat gtg aca act tta gca cat cgt cgt ggt gat caa agg      466
Ser Met Glu Asn Val Thr Thr Leu Ala His Arg Arg Gly Asp Gln Arg
75                  80                  85                  90

aaa acg cta aga gag gaa gat gat ttt gcg gtt cct gta tat gtt aat      514
Lys Thr Leu Arg Glu Glu Asp Asp Phe Ala Val Pro Val Tyr Val Asn
```

```
                95                  100                 105

gat agc tca aga aga ttt caa tgt cct ctt gaa aag tca gca tcg ggt      562
Asp Ser Ser Arg Arg Phe Gln Cys Pro Leu Glu Lys Ser Ala Ser Gly
            110                 115                 120

tgt gaa aga gtt aat gct tct tgt gag aca gag tct aca agt agt agg      610
Cys Glu Arg Val Asn Ala Ser Cys Glu Thr Glu Ser Thr Ser Ser Arg
        125                 130                 135

tta gac cat gaa act gga gtg atg gaa act gat gat gga gtt gaa tct      658
Leu Asp His Glu Thr Gly Val Met Glu Thr Asp Asp Gly Val Glu Ser
    140                 145                 150

cat ggc aat cct aat gac gtc gat gat gat gat gat gat gat tcg ata      706
His Gly Asn Pro Asn Asp Val Asp Asp Asp Asp Asp Asp Asp Ser Ile
155                 160                 165                 170

tcc agc ata gac gtc tct tct gat gaa gtt gtg gga gta tta ggt caa      754
Ser Ser Ile Asp Val Ser Ser Asp Glu Val Val Gly Val Leu Gly Gln
                175                 180                 185

aac cgk ttc tgg aga gca agg aar gct atk gcc aag aa  gtycctcata      802
Asn Arg Phe Trp Arg Ala Arg Lys Ala Xaa Ala Lys Asn
            190                 195

gacttttggt gaactggtaa ggaatttttt gggtctttct ctgctgtttt aatgcttaaa    862

tgatgcaatg gtttgctcac aacatacata tatgattata actctgcttt atattttgaa    922

aaagaccaga tttggtttat ttttgattga gaagtgataa ttttttagtg aagaaacccc    982

ctgactcctc caaaaattga aggttcccgc cgagacagtt aatggatttt gcatctgctt   1042

gctggaacat gtccctgtcc ctgtctcggt ttggtatttg cttttattct gcattttccc   1102

ttcttgtcat tcaacgggtt gaaccaggta gttaaccata cataaagcta gttatgtgtc   1162

ttatgaaaat gaagaattat agtagcagag gttgtaaact atggagtttt ctatggattt   1222

tagactctgt tactcaggtt ttaaggttct atgtaaggta tcaattaaac ccacccttg   1282

cataatgtct tcagtttttc ttcttctatt atttatgcct ttctctgtgt tttttgacgc   1342

attgatttgc ttcttcatca ttgttggtta gaggcttctt gcttcttttt ttttccgatt   1402

ctactgttct attatttgtt caaccgaaac tatatctatc tctctttgtg gaacttttct   1462

tatgggtcat cttcttgatc tgaccttgtt tctccgtaac ag t caa caa aga ata    1517
                                                Gln Gln Arg Ile
                                                200

ttt gcg gtt caa tta ttt gag ttg cac agg ctr att aag gtaaaactca      1566
Phe Ala Val Gln Leu Phe Glu Leu His Arg Xaa Ile Lys
    205                 210                 215

ttcagaaaac ttctcctacg tttcatgaat atttgttttg tgcaaaccta gtcaactgta   1626
```

```
ctttgttttc actataatca ag gtt caa aga ctt att gct tca tca tcg gat    1678
                        Val Gln Arg Leu Ile Ala Ser Ser Ser Asp
                                    220                 225

gtc ttg ctc gat gag atc agt tat ctt gga aat gtt cca gtg aag aag    1726
Val Leu Leu Asp Glu Ile Ser Tyr Leu Gly Asn Val Pro Val Lys Lys
            230                 235                 240

ctt ctt ccc tct gaa ttt ata tta aag cct cct cct cta cca cag gtt    1774
Leu Leu Pro Ser Glu Phe Ile Leu Lys Pro Pro Pro Leu Pro Gln Val
        245                 250                 255

acc aaa cac aga agc agc gac tcc gag aag act gac caa aat aaa atg    1822
Thr Lys His Arg Ser Ser Asp Ser Glu Lys Thr Asp Gln Asn Lys Met
    260                 265                 270

gaa tcc tca gct gag aac gta gtc ggg aag tcg tca aac caa ggt cag    1870
Glu Ser Ser Ala Glu Asn Val Val Gly Lys Ser Ser Asn Gln Gly Gln
275                 280                 285                 290

cag cat caa ccg tcc aac tac atg cct ttt gcg agc aac cca cca gct    1918
Gln His Gln Pro Ser Asn Tyr Met Pro Phe Ala Ser Asn Pro Pro Ala
                295                 300                 305

gca aat gga tgt tac tat cct cct cag cat cct cct ccc tct gga gga    1966
Ala Asn Gly Cys Tyr Tyr Pro Pro Gln His Pro Pro Pro Ser Gly Gly
            310                 315                 320

aat cag                                                            1972
Asn Gln
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<210> 61
<211> 324
<212> PRT
<213> Brassica sp.

<220>
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<222> (188)..(188)
<223> Xaa = uncertain amino acid residue

<220>
<221> misc_feature
<222> (194)..(194)
<223> Xaa = uncertain amino acid residue

<220>
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<223> Xaa = uncertain amino acid residue

<220>
<221> misc_feature
<222> (214)..(214)
<223> Xaa = uncertain amino acid residue

<400> 61

Lys Gly Gly Gly Pro Arg Ala Pro Pro Arg Asn Lys Met Ala Leu Tyr
1 5 10 15

Glu His Leu Thr Thr Pro Ser His Arg Phe Thr Asp His Ser Ser Ser
20 25 30

Pro Arg His Thr Asn Thr Leu Phe Pro Pro Pro Pro Gly Pro Ser Asn
35 40 45

Gln Pro Cys Gly Val Glu Arg Asn Leu Thr Ser Gln His Leu Asp Ser
50 55 60

Ser Ala Ser Gly His Val Thr Gln Met Ser Ser Met Glu Asn Val Thr
65 70 75 80

Thr Leu Ala His Arg Arg Gly Asp Gln Arg Lys Thr Leu Arg Glu Glu
85 90 95

Asp Asp Phe Ala Val Pro Val Tyr Val Asn Asp Ser Ser Arg Arg Phe
100 105 110

Gln Cys Pro Leu Glu Lys Ser Ala Ser Gly Cys Glu Arg Val Asn Ala
115 120 125

Ser Cys Glu Thr Glu Ser Thr Ser Ser Arg Leu Asp His Glu Thr Gly
130 135 140

Val Met Glu Thr Asp Asp Gly Val Glu Ser His Gly Asn Pro Asn Asp
145 150 155 160

Val Asp Asp Asp Asp Asp Asp Asp Ser Ile Ser Ser Ile Asp Val Ser
165 170 175

Ser Asp Glu Val Val Gly Val Leu Gly Gln Asn Xaa Phe Trp Arg Ala
180 185 190

Arg Xaa Ala Xaa Ala Lys Asn Gln Gln Arg Ile Phe Ala Val Gln Leu

```
        195                 200                 205

Phe Glu Leu His Arg Xaa Ile Lys Val Gln Arg Leu Ile Ala Ser Ser
    210                 215                 220

Ser Asp Val Leu Leu Asp Glu Ile Ser Tyr Leu Gly Asn Val Pro Val
225                 230                 235                 240

Lys Lys Leu Leu Pro Ser Glu Phe Ile Leu Lys Pro Pro Pro Leu Pro
                245                 250                 255

Gln Val Thr Lys His Arg Ser Ser Asp Ser Glu Lys Thr Asp Gln Asn
            260                 265                 270

Lys Met Glu Ser Ser Ala Glu Asn Val Val Gly Lys Ser Ser Asn Gln
        275                 280                 285

Gly Gln Gln His Gln Pro Ser Asn Tyr Met Pro Phe Ala Ser Asn Pro
    290                 295                 300

Pro Ala Ala Asn Gly Cys Tyr Tyr Pro Pro Gln His Pro Pro Pro Ser
305                 310                 315                 320

Gly Gly Asn Gln
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<210> 62
<211> 505
<212> DNA
<213> Brassica

<220>
<221> exon
<222> (2)..(505)
<223>

<400> 62

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a ccc ggt cca gat ccg ggg cac acg ggg ccg gtc tgt gga ggg tat tat     49
  Pro Gly Pro Asp Pro Gly His Thr Gly Pro Val Cys Gly Gly Tyr Tyr
  1               5                  10                  15

ggt cat ttc atg cct gca cca atg ttc atg ggt ggt ggt ggt ggt cag       97
Gly His Phe Met Pro Ala Pro Met Phe Met Gly Gly Gly Gly Gly Gln
            20                  25                  30

cct cct ccg ttt cac ccg ggc atg gga ttc cya tct cat ggt aat ggc      145
Pro Pro Pro Phe His Pro Gly Met Gly Phe Xaa Ser His Gly Asn Gly
```

```
        35                  40                  45

tac ttt cct cca tat ggt ggt atc atg atg aac cct tac tat tcc gga      193
Tyr Phe Pro Pro Tyr Gly Gly Ile Met Met Asn Pro Tyr Tyr Ser Gly
    50                  55                  60

cra caa caa caa caa caa ccc aat gag caa atg aac aac aac atc caa      241
Xaa Gln Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Asn Asn Ile Gln
65                  70                  75                  80

caa cag agc tca gtg aat gaa gcg act tca caa caa caa cag cca acg      289
Gln Gln Ser Ser Val Asn Glu Ala Thr Ser Gln Gln Gln Gln Pro Thr
                85                  90                  95

aaa tct tat cct cgg gct aaa aag agc agg caa gag gga atc tct ggt      337
Lys Ser Tyr Pro Arg Ala Lys Lys Ser Arg Gln Glu Gly Ile Ser Gly
            100                 105                 110

aag aag aag tcc ttt caa cca ttc tca gcg gtt gat gat gtt cat gat      385
Lys Lys Lys Ser Phe Gln Pro Phe Ser Ala Val Asp Asp Val His Asp
        115                 120                 125

gac aag atc aac aat gct gca caa cct act gag gaa atg atg acg aca      433
Asp Lys Ile Asn Asn Ala Ala Gln Pro Thr Glu Glu Met Met Thr Thr
    130                 135                 140

acc aca acc aca aca aca act gtg act cag aca acg aga gat gga gca      481
Thr Thr Thr Thr Thr Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Ala
145                 150                 155                 160

gga gtg acg aga gtg atc aag gtg                                     505
Gly Val Thr Arg Val Ile Lys Val
                165
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<210> 63
<211> 168
<212> PRT
<213> Brassica sp.

<220>
<221> misc_feature
<222> (43)..(43)
<223> Xaa = uncertain amino acid residue

<220>
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<222> (65)..(65)
<223> Xaa = uncertain amino acid residue

<400> 63

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Pro Gly Pro Asp Pro Gly His Thr Gly Pro Val Cys Gly Gly Tyr Tyr
1               5                   10                  15
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Gly His Phe Met Pro Ala Pro Met Phe Met Gly Gly Gly Gly Gly Gln
            20                  25                  30

Pro Pro Pro Phe His Pro Gly Met Gly Phe Xaa Ser His Gly Asn Gly
        35                  40                  45

Tyr Phe Pro Pro Tyr Gly Gly Ile Met Met Asn Pro Tyr Tyr Ser Gly
    50                  55                  60

Xaa Gln Gln Gln Gln Pro Asn Glu Gln Met Asn Asn Asn Ile Gln
65                  70                  75                  80

Gln Gln Ser Ser Val Asn Glu Ala Thr Ser Gln Gln Gln Gln Pro Thr
                85                  90                  95

Lys Ser Tyr Pro Arg Ala Lys Lys Ser Arg Gln Glu Gly Ile Ser Gly
            100                 105                 110

Lys Lys Lys Ser Phe Gln Pro Phe Ser Ala Val Asp Asp Val His Asp
        115                 120                 125

Asp Lys Ile Asn Asn Ala Ala Gln Pro Thr Glu Glu Met Met Thr Thr
    130                 135                 140

Thr Thr Thr Thr Thr Thr Thr Val Thr Gln Thr Thr Arg Asp Gly Ala
145                 150                 155                 160

Gly Val Thr Arg Val Ile Lys Val
                165
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<210> 64
<211> 36
<212> DNA
<213> synthetic oligonucleotide

<220>
<221> misc_feature
<222> (28)..(28)
<223> n = any nucleic acid residue

<400> 64
tgttatgtct ccttctgaag gactgrtnta yaarcc 36

<210> 65

<211> 35
<212> DNA
<213> synthetic oligonucleotide

<220>
<221> misc_feature
<222> (30)..(30)
<223> n = any nucleic acid

<220>
<221> misc_feature
<222> (33)..(33)
<223> n = any nucleic acid

<400> 65
gcagattcag aagcagttct agcaktrtgn ggnac 35

<210> 66
<211> 35
<212> DNA
<213> synthetic oligonucleotide

<220>
<221> misc_feature
<222> (33)..(33)
<223> n = any nucleic acid

<400> 66
caaagagttt ttgctgttca agttttygar ytnca 35

<210> 67
<211> 20
<212> DNA
<213> synthetic oligonucleotide

<400> 67
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